

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:22:25 ; Search time 133.103 Seconds  
(without alignments)  
579.640 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579

Sequence: 1 MNKLYIGNLSENAAPSDLES.....VKHQOQKALSGPQPSRRK 579

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

A\_Geneseq\_101002:\*

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- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	100.0	579	21 AAB11328	Human lung cancer-
2	579	100.0	579	23 AAB74960	Human lung cancer-
3	377	65.1	579	21 AAB11365	Human lung cancer
4	377	65.1	579	23 AAB74997	Human lung cancer
5	377	65.1	579	23 AAB75053	Human lung tumour
6	377	65.1	579	23 AAB75054	Human lung tumour
7	376	64.9	586	23 AAB75048	Human lung tumour
8	148	23.7	619	22 AAB21963	Novel human diagno
9	89	17.1	148	22 AAB21962	Novel human diagno
10	93	16.1	93	22 AAB78238	Human bone marrow

11	93	16.1	93	22 AAB38501	Peptide #12338 enc
12	65	11.2	583	22 AAG12592	Novel human diagno
13	45	7.8	45	22 AAB84327	Peptide #10933 enc
14	45	7.8	45	22 AAB64356	Human brain expres
15	45	7.8	45	22 AAM37315	Peptide #11352 enc
16	37	6.4	209	22 AAG12593	Novel human diagno
17	37	6.4	266	22 AAG12593	Novel human diagno
18	36	6.2	577	20 AAB30649	A murine c-myc cod
19	26	4.5	39	22 AAB21960	Novel human diagno
20	24	4.1	261	22 AAB16161	Human novel secret
21	24	4.1	319	22 AAB93826	Human polypeptide,
22	20	3.5	20	23 AAB75024	Human lung tumour
23	20	3.5	20	23 AAB75025	Human lung tumour
24	20	3.5	20	23 AAB75026	Human lung tumour
25	20	3.5	20	23 AAB75027	Human lung tumour
26	20	3.5	20	23 AAB75028	Human lung tumour
27	20	3.5	20	23 AAB75029	Human lung tumour
28	20	3.5	20	23 AAB75030	Human lung tumour
29	20	3.5	20	23 AAB75031	Human lung tumour
30	20	3.5	20	23 AAB75032	Human lung tumour
31	20	3.5	20	23 AAB75033	Human lung tumour
32	20	3.5	20	23 AAB75036	Human lung tumour
33	20	3.5	20	23 AAB75037	Human lung tumour
34	20	3.5	20	23 AAB75038	Human lung tumour
35	20	3.5	20	23 AAB75039	Human lung tumour
36	20	3.5	20	23 AAB75040	Human lung tumour
37	20	3.5	20	23 AAB75041	Human lung tumour
38	20	3.5	20	23 AAB75042	Human lung tumour
39	20	3.5	20	23 AAB75043	Human lung tumour
40	20	3.5	20	23 AAB75044	Human lung tumour
41	20	3.5	20	23 AAB75045	Human lung tumour
42	20	3.5	20	23 AAB75046	Human lung tumour
43	20	3.5	20	23 AAB75058	Human lung tumour
44	20	3.5	20	23 AAB75060	Human lung tumour
45	20	3.5	20	23 AAB75061	Human lung tumour

#### ALIGNMENTS

RESULT 1					
AAB11328 standard; Protein; 579 AA.					
ID	AC	AB11328;			
XX	XX				
XX	XX	21-FEB-2001 (first entry)			
XX	XX				
XX	XX	Human lung cancer-associated protein L523S.			
XX	XX				
XX	XX	Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;			
XX	XX	vaccline; detection.			
XX	XX				
XX	XX	Homo sapiens.			
XX	XX				
XX	XX	WO200061612-A2.			
XX	XX	19-OCT-2000.			
XX	XX				
XX	XX	03-APR-2000; 2000MO-US08896.			
XX	XX				
XX	XX	02-APR-1999; 99US-0285479.			
XX	XX	17-DEC-1999; 99US-0466396.			
XX	XX	30-DEC-1999; 99US-0476496.			
XX	XX	10-JAN-2000; 2000US-0480884.			
XX	XX	22-FEB-2000; 2000US-0510376.			
XX	XX				
XX	XX	(CORI-) CORIXA CORP.			
XX	XX				
XX	XX	Wang T, Fan L;			
XX	XX				
XX	XX	WPI, 2000-628399/60.			
XX	XX				
XX	XX	N-PSDB; AAC65900.			
XX	XX				

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor  
PT protein is used for detecting and monitoring progression of lung cancer  
in a patient -

Claim 3: Page 186-188; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which  
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)  
CC which have cytostatic activity. The polypeptides and polynucleotides are  
CC used in compositions and vaccines to inhibit the development of cancer,  
CC especially lung cancer, in a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.

XX Sequence 579 AA:

Query Match 100.0%; Score 579; DB 21; Length 579;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
QY 61 IELGKPIEVEHSPVKRQRIKLOIRNIPHLQWELVDSLLVYGVVESCQVNTDSETA 120  
DB 61 IELGKPIEVEHSPVKRQRIKLOIRNIPHLQWELVDSLLVYGVVESCQVNTDSETA 120  
QY 121 VVNTVSSKDOARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLQOPRGRGLGGRGSS 180  
DB 121 VVNTVSSKDOARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLQOPRGRGLGGRGSS 180  
QY 181 RQSGPVSQKQPCDPLRLLLVPTQFVGAIIGKEGATTIRNITKOTQSKIDVHRKENAGAA 240  
DB 181 RQSGPVSQKQPCDPLRLLLVPTQFVGAIIGKEGATTIRNITKOTQSKIDVHRKENAGAA 240  
QY 241 EKSTILLSTPEGTSACKSILEIMHKEADIKFTEIEIPKLILAHNNVGRLLGKGRNLK 300  
DB 241 EKSTILLSTPEGTSACKSILEIMHKEADIKFTEIEIPKLILAHNNVGRLLGKGRNLK 300  
QY 301 KIEQDTTKITISPLQELILYNPERTIVKGNVETCAKAEIEIMKKIRRESYENDIASNML 360  
DB 301 KIEQDTTKITISPLQELILYNPERTIVKGNVETCAKAEIEIMKKIRRESYENDIASNML 360  
QY 361 QAHLIPGLMLNALGLPPTSGMPPTSGPPSAMTPPYPOFQSETEYVHOPIALSVGAI 420  
DB 361 QAHLIPGLMLNALGLPPTSGMPPTSGPPSAMTPPYPOFQSETEYVHOPIALSVGAI 420  
QY 421 IGKOGHTRKQLSRFRAGASIKIADAEAPDAKVMVITITPEPAFKAOGRIYKIKENFV 480  
DB 421 IGKOGHTRKQLSRFRAGASIKIADAEAPDAKVMVITITPEPAFKAOGRIYKIKENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVMELONLSAEVVPVRODTPDENDQVYVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVMELONLSAEVVPVRODTPDENDQVYVKIT 540  
QY 541 GHFYACQVAORRIGQELITQVKHQOQKALQSGPPQSRK 579  
DB 541 GHFYACQVAORRIGQELITQVKHQOQKALQSGPPQSRK 579

RESULT 2  
ABB74960 ID ABB74960 standard; Protein: 579 AA.  
XX ABB74960;  
XX AC  
XX 01-MAY-2002 (first entry)

XX Human lung tumour L523S protein sequence SEQ ID NO:176.  
XX Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
XX Immune response.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

XX 15-SEP-2000; 2000US-0662786.

XX 09-OCT-2000; 2000US-0685696.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

XX McNeill PD, Fanger N, Retter MW, Marnettakis M, Fanger GR;

XX Veddyck TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

XX N-PSDB; ABL49119.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

XX lung cancer or stimulating an immune response -

XX Example 2: Page 267-268; 374pp; English.

XX The present invention describes human lung tumor proteins. Human lung

XX tumor proteins and polynucleotides have cytostatic and immunostimulant

XX activities, and can be used in vaccine production. Compositions

XX comprising the lung tumor proteins, polynucleotides, antibodies,

XX fusion proteins, T cell populations, or antigen presenting cells that

XX express the lung tumor proteins are useful for treating lung cancer or

XX stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

XX ABB75070 represent sequences used in the exemplification of the present

XX invention.

XX Sequence 579 AA:

XX Query Match 100.0%; Score 579; DB 23; Length 579;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
DB 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
QY 61 IELGKPIEVEHSPVKRQRIKLOIRNIPHLQWELVDSLLVYGVVESCQVNTDSETA 120  
DB 61 IELGKPIEVEHSPVKRQRIKLOIRNIPHLQWELVDSLLVYGVVESCQVNTDSETA 120  
QY 121 VVNTVSSKDOARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLQOPRGRGLGGRGSS 180  
DB 121 VVNTVSSKDOARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLQOPRGRGLGGRGSS 180  
QY 181 RQSGPVSQKQPCDPLRLLLVPTQFVGAIIGKEGATTIRNITKOTQSKIDVHRKENAGAA 240  
DB 181 RQSGPVSQKQPCDPLRLLLVPTQFVGAIIGKEGATTIRNITKOTQSKIDVHRKENAGAA 240  
QY 241 EKSTILLSTPEGTSACKSILEIMHKEADIKFTEIEIPKLILAHNNVGRLLGKGRNLK 300  
DB 241 EKSTILLSTPEGTSACKSILEIMHKEADIKFTEIEIPKLILAHNNVGRLLGKGRNLK 300  
QY 301 KIEQDTTKITISPLQELILYNPERTIVKGNVETCAKAEIEIMKKIRRESYENDIASNML 360  
DB 301 KIEQDTTKITISPLQELILYNPERTIVKGNVETCAKAEIEIMKKIRRESYENDIASNML 360

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Db 301 KIEDDTDKITISPLQELTYLNEPRTITVKGAVETCAKAEIEIMKIRESEYENDIASMNL 360
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Db 361 QAHILPGLNINLALGLPPTSGMPPTSGPSSAMTPPYQPFQSETEYHOFIPALSYGAI 420
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Db 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMVITITGPPEAOFKAGRTYKIKENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVVPDQTPDENDDVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVVPDQTPDENDDVYVKIT 540
Qy 541 GHFYACQVAORAKIOEILITGVKHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVAORAKIOEILITGVKHQOQKALQSGPPQSRK 579

```

## RESULT 3

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ID AAB11365 standard; Protein; 579 AA.
AC AAB11365;
DT 21-FEB-2001 (first entry)
DE Human lung cancer associated antigen L523S.
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
  vaccine; detection.
OS Homo sapiens.
PM W0200061612-A2.
PD 19-OCT-2000.
PF 03-APR-2000; 2000MO-US08896.
PR 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
PA (CORI-) CORIXA CORP.
PI Wang T, Fan L;
DR WPI: 2000-628399/60.
DR N-PSDB; AAC66035.

```

Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient -

Claim 3; Page 259-261; 261pp: English.

This invention describes a novel isolated polypeptide (1) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.

Sequence 579 AA;

Query Match 65.1%; Score 377; DB 21; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 2; Indels 0; Gaps 0;

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Qy 61 TELHGKPIEVESHVPPKROKRIKQIINIPPHLOMEVLDLSLYGVVESCQVNTDSETA 120
Db 61 TELHGKPIEVESHVPPKROKRIKQIINIPPHLOMEVLDLSLYGVVESCQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFOLNEFTLKVAYIPDEMAAQNPLQOPRGRGIGQSGSS 180
Db 121 VVNTYSSKQARQALDKLNGFOLNEFTLKVAYIPDEMAAQNPLQOPRGRGIGQSGSS 180
Qy 181 RQSGPQSVSKQKPCDPLRLVPTQFVGAIIKKEGATIRNTKOTQSKIDVHRKENAGAA 240
Db 181 RQSGPQSVSKQKPCDPLRLVPTQFVGAIIKKEGATIRNTKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPEGTSACKSITLIMKEADIKFTBEIPKILAHNNEFYGRILGKEGRNLK 300
Db 241 EKSTITLSTPEGTSACKSITLIMKEADIKFTBEIPKILAHNNEFYGRILGKEGRNLK 300
Qy 301 KIEDDTDKITISPLQELTYLNEPRTITVKGAVETCAKAEIEIMKIRESEYENDIASMNL 360
Db 301 KIEDDTDKITISPLQELTYLNEPRTITVKGAVETCAKAEIEIMKIRESEYENDIASMNL 360
Qy 361 QAHILPGLNINLALGLPPTSGMPPTSGPSSAMTPPYQPFQSETEYHOFIPALSYGAI 420
Db 361 QAHILPGLNINLALGLPPTSGMPPTSGPSSAMTPPYQPFQSETEYHOFIPALSYGAI 420
Qy 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMVITITGPPEAOFKAGRTYKIKENFV 480
Db 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMVITITGPPEAOFKAGRTYKIKENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVVPDQTPDENDDVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVVPDQTPDENDDVYVKIT 540
Qy 541 GHFYACQVAORAKIOEILITGVKHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVAORAKIOEILITGVKHQOQKALQSGPPQSRK 579

```

## RESULT 4

ABB74997 standard; Protein; 579 AA.

ABB74997;

01-MAY-2002 (first entry)

Human lung tumour L523S protein sequence SEQ ID NO:348.

Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine; immune response.

Homo sapiens.

W0200200174-A2.

03-JAN-2002.

28-JUN-2001; 2001MO-US21065.

28-JUN-2000; 2000US-0606421.

02-AUG-2000; 2000US-0630940.

21-AUG-2000; 2000US-06437897.

13-SEP-2000; 2000US-0662786.

09-OCT-2000; 2000US-0683696.

12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retter MW, Marnierakis M, Fanger GR;  
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
 XX  
 DR MPI: 2002-090513/12.  
 DR N-PSDB; ABL49254.  
 XX  
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
 PT lung cancer or stimulating an immune response -  
 XX  
 PS Example 2; Page 330-332; 374pp; English.  
 XX  
 CC The present invention describes human lung tumour proteins. Human lung  
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production. Compositions  
 CC comprising the lung tumour proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumour proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to  
 CC ABL75070 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 579 AA:

Query Match 65.1%; Score 377; DB 23; Length 579;  
 Best local similarity 99.7%; Pred. No. 0;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSCK 60  
 DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSCK 60  
 QY 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLSLLVQGVSECEQVNTDSETA 120  
 DB 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLSLLVQGVSECEQVNTDSETA 120  
 QY 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAVIPDEMAAQNPLQOPRRKGLQGRSS 180  
 DB 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAVIPDEMAAQNPLQOPRRKGLQGRSS 180  
 QY 181 RQSGPSVSKOKPCDLPLRLVPTQFVGAIIKSGATIRNITQTSKIDVHRKEMAGAA 240  
 DB 181 RQSGPSVSKOKPCDLPLRLVPTQFVGAIIKSGATIRNITQTSKIDVHRKEMAGAA 240  
 QY 241 EKSTILSTPGTSAACKSILEIMHREKADIKFTEELPLKILAHNNFVGRIGKGRNLK 300  
 DB 241 EKSTILSTPGTSAACKSILEIMHREKADIKFTEELPLKILAHNNFVGRIGKGRNLK 300  
 QY 301 KTEODTTRITISPLQELTLYNPERTIVKGNVETCAKAEELMKKIRESYENDIASMNL 360  
 DB 301 KTEODTTRITISPLQELTLYNPERTIVKGNVETCAKAEELMKKIRESYENDIASMNL 360  
 QY 361 QAHLIPGLNLNALGLPPTSGMPPTSGPPSAMTPPYPOEOSTETVHQETPALSGAI 420  
 DB 361 QAHLIPGLNLNALGLPPTSGMPPTSGPPSAMTPPYPOEOSTETVHQETPALSGAI 420  
 QY 421 IKGQOHIKOLSRFAGASIKIAFAEPDAKVRWYIITGPEDAFKAGKIRGKIKENFV 480  
 DB 421 IKGQOHIKOLSRFAGASIKIAFAEPDAKVRWYIITGPEDAFKAGKIRGKIKENFV 480  
 QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTIVNELONLSAEVVVPRDQTDENDOVVYK 540  
 DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTIVNELONLSAEVVVPRDQTDENDOVVYK 540  
 QY 541 GHEYACQVAORRIGIELITVYKQHQQOAKALQSGPPSSRRK 579  
 DB 541 GHEYACQVAORRIGIELITVYKQHQQOAKALQSGPPSSRRK 579

RESULT 5  
 ABB75053  
 ID ABB75053 standard; Protein: 579 AA.  
 XX  
 AC ABB75053;  
 XX  
 DT 01-MAY-2002 (first entry)  
 XX  
 DE Human lung tumour L523S recombinant protein sequence SEQ ID NO:446.  
 XX  
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200200174-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 28-JUN-2001; 2001WO-US21065.  
 XX  
 PR 28-JUN-2000; 2000US-0606421.  
 PR 02-AUG-2000; 2000US-0630940.  
 PR 21-AUG-2000; 2000US-0643597.  
 PR 15-SEP-2000; 2000US-0662786.  
 PR 09-OCT-2000; 2000US-0685696.  
 PR 12-DEC-2000; 2000US-0735705.  
 PR 07-MAY-2001; 2001US-0850716.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retter MW, Marnierakis M, Fanger GR;  
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
 XX  
 DR MPI: 2002-090513/12.  
 DR N-PSDB; ABL49297.  
 XX  
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
 PT lung cancer or stimulating an immune response -  
 XX  
 PS Claim 2; Page 365-367; 374pp; English.  
 XX  
 CC The present invention describes human lung tumour proteins. Human lung  
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production. Compositions  
 CC comprising the lung tumour proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumour proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to  
 CC ABL75070 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 579 AA:

Query Match 65.1%; Score 377; DB 23; Length 579;  
 Best local similarity 99.7%; Pred. No. 0;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSCK 60  
 DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSCK 60  
 QY 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLSLLVQGVSECEQVNTDSETA 120  
 DB 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLSLLVQGVSECEQVNTDSETA 120  
 QY 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAVIPDEMAAQNPLQOPRRKGLQGRSS 180  
 DB 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAVIPDEMAAQNPLQOPRRKGLQGRSS 180  
 QY 181 RQSGPSVSKOKPCDLPLRLVPTQFVGAIIKSGATIRNITQTSKIDVHRKEMAGAA 240  
 DB 181 RQSGPSVSKOKPCDLPLRLVPTQFVGAIIKSGATIRNITQTSKIDVHRKEMAGAA 240



DB 181 RQSPGVSVKQKPCDPLRLVPTQFVGAIIGKCATIRNTKOTSKIDVHRKENGAA 240  
 QY 241 EKSTILLSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNVGRIGKEGRNLK 300  
 DB 241 EKSTILLSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNVGRIGKEGRNLK 300  
 QY 301 KIEODDTKITTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESEYNDIASMNL 360  
 DB 301 KIEODDTKITTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESEYNDIASMNL 360  
 QY 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 DB 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAOFKAAGRILYGIKEENFV 480  
 DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAOFKAAGRILYGIKEENFV 480  
 QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELQNLSSAEVVPDPTPDENDQVYVKIT 540  
 DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELQNLSSAEVVPDPTPDENDQVYVKIT 540  
 QY 541 GHFYACOVAQRKIOELITGVKQHQQOKALQSGPPQSRK 579  
 DB 541 GHFYACOVAQRKIOELITGVKQHQQOKALQSGPPQSRK 579

## RESULT 6

ABB75054  
 ID ABB75054 standard; Protein: 579 AA.

AC ABB75054;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L523s recombinant protein sequence SEQ ID NO:449.

KW Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

IM Immune response.

OS Homo sapiens.

PN WO200200174-A2.

PD 03-JAN-2002.

PF 28-JUN-2001; 2001WO-US21065.

PR 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

PA (CORI-) CORIXA CORP.

PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Fanger N, Retter MM, Marnierakis M, Fanger GR;

PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

PS WPI: 2002-090513/12.

PS N-PSDB; ABL49299.

CC The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies, CC fusion proteins, T cell populations, or antigen presenting cells that CC express the lung tumour proteins are useful for treating lung cancer or CC stimulating an immune response. ABL48959 to ABL49300 and ABB7946 to CC ABB75070 represent sequences used in the exemplification of the present CC invention.

XX Sequence 579 AA;

SO Query Match 65.1%; Score 377; DB 23; Length 579;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKGVAFVDCDDSMALKATEALSGK 60  
 DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKGVAFVDCDDSMALKATEALSGK 60  
 QY 61 IELHGKPIEVEHSPKRRQRIKIQIRNIPHLQWEVLDSLVOYGVESEQVNTDSETA 120  
 DB 61 IELHGKPIEVEHSPKRRQRIKIQIRNIPHLQWEVLDSLVOYGVESEQVNTDSETA 120  
 QY 121 VVWVYSSKQDQARQALDKNGFQLENTLKVAYIPDEMAQONLQOPRGRRIGQGGSS 180  
 DB 121 VVWVYSSKQDQARQALDKNGFQLENTLKVAYIPDEMAQONLQOPRGRRIGQGGSS 180  
 QY 121 VVWVYSSKQDQARQALDKNGFQLENTLKVAYIPDEMAQONLQOPRGRRIGQGGSS 180  
 DB 121 VVWVYSSKQDQARQALDKNGFQLENTLKVAYIPDEMAQONLQOPRGRRIGQGGSS 180  
 QY 181 RQSPGVSVKQKPCDPLRLVPTQFVGAIIGKCATIRNTKOTSKIDVHRKENGAA 240  
 DB 181 RQSPGVSVKQKPCDPLRLVPTQFVGAIIGKCATIRNTKOTSKIDVHRKENGAA 240  
 QY 241 EKSTILLSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNVGRIGKEGRNLK 300  
 DB 241 EKSTILLSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNVGRIGKEGRNLK 300  
 QY 301 KIEODDTKITTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESEYNDIASMNL 360  
 DB 301 KIEODDTKITTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESEYNDIASMNL 360  
 QY 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 DB 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAOFKAAGRILYGIKEENFV 480  
 DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAOFKAAGRILYGIKEENFV 480  
 QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELQNLSSAEVVPDPTPDENDQVYVKIT 540  
 DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELQNLSSAEVVPDPTPDENDQVYVKIT 540  
 QY 541 GHFYACOVAQRKIOELITGVKQHQQOKALQSGPPQSRK 579  
 DB 541 GHFYACOVAQRKIOELITGVKQHQQOKALQSGPPQSRK 579

## RESULT 7

ABB75048  
 ID ABB75048 standard; Protein: 586 AA.

AC ABB75048;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L523s recombinant protein sequence SEQ ID NO:427.

KW Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

IM Immune response.

OS Homo sapiens.

PN WO200200174-A2.

PD 03-JAN-2002.

XX

PF 28-JUN-2001; 2001WO-US21065.  
 XX 28-JUN-2000; 2000US-0606421.  
 PR 02-AUG-2000; 2000US-0630940.  
 PR 21-AUG-2000; 2000US-0643597.  
 PR 15-SEP-2000; 2000US-0662786.  
 PR 09-OCT-2000; 2000US-0685696.  
 PR 12-DEC-2000; 2000US-0735705.  
 PR 07-MAY-2001; 2001US-0850716.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retter MW, Marnierals M, Fanger GR;  
 PI Vedvyck JS, Carter D, Watanabe Y, Peckham DW;  
 XX  
 DR WPI: 2002-090513/12.  
 DR N-PSDB: ABL49283.  
 XX  
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
 PT lung cancer or stimulating an immune response -  
 XX  
 PS Claim 2; Page 354-355; 374pp; English.  
 XX  
 CC The present invention describes human lung tumour proteins, human lung  
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production, compositions  
 CC comprising the lung tumour proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumour proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL4935 to ABL49300 and ABL4946 to  
 CC ABL495070 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 586 AA;  
 XX  
 Query Match 64.9%; Score 376; DB 23; Length 586;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 NKLTYGNLSNNAAPSDLESIFKDAKIPVSGPELVYTGAFVDCDESMALKAIEALSGKI 61  
 DB 9 NKLTYGNLSNNAAPSDLESIFKDAKIPVSGPELVYTGAFVDCDESMALKAIEALSGKI 68  
 QY 62 ELHGKPIEVEHSVPRKRIKRLQIRNIPHLQMEVLDLVOYGVESCEQVNDSEYAV 121  
 DB 69 ELHGKPIEVEHSVPRKRIKRLQIRNIPHLQMEVLDLVOYGVESCEQVNDSEYAV 128  
 QY 122 VAVTYSKDOARQALDKLNGFOLNFTLVAVIIPDEMAAQNPILOPRGRGIGOGSSR 181  
 DB 129 VAVTYSKDOARQALDKLNGFOLNFTLVAVIIPDEMAAQNPILOPRGRGIGOGSSR 188  
 QY 182 GSGPSGVSKOKPCDPLRLVPOFGALIGEGATINIKOTQSKIDVHKENAGAAE 241  
 DB 189 GSGPSGVSKOKPCDPLRLVPOFGALIGEGATINIKOTQSKIDVHKENAGAAE 248  
 QY 242 KSITLSTPEGSTAACKSILEIHKKAQDIKTEEPILKAHNNFVGRLLIGEGNNLK 301  
 DB 249 KSITLSTPEGSTAACKSILEIHKKAQDIKTEEPILKAHNNFVGRLLIGEGNNLK 308  
 QY 302 IEODTDKITITISPLQELTLVNPRTTVKGVNETCAKAEEMIKRESYENDIASMNQ 361  
 DB 309 IEODTDKITITISPLQELTLVNPRTTVKGVNETCAKAEEMIKRESYENDIASMNQ 368  
 QY 362 AHLIPGLNLNLGLFPTSGMPPTSGPSAMTPYPOFQESSETYHOFIPLASGATII 421  
 DB 369 AHLIPGLNLNLGLFPTSGMPPTSGPSAMTPYPOFQESSETYHOFIPLASGATII 428  
 QY 422 GKGOGHITKOLSRFAGASIKTAPEADAVRVAVIITGPEKQFAQGRITGKKEENFVS 481  
 DB 429 GKGOGHITKOLSRFAGASIKTAPEADAVRVAVIITGPEKQFAQGRITGKKEENFVS 488  
 QY 482 PKEEVKLEAHIRVPSFAAGVIGKGGKTVNELONLSAEEVAVPRDQTPDENDDVAVKING 541

DB 489 PKEEVKLEAHIRVPSFAAGVIGKGGKTVNELONLSAEEVAVPRDQTPDENDDVAVKING 548  
 QY 542 HFIACQVNAQRKIQEILTYVKOHQOQAKLOSPPQSRK 579  
 DB 549 HFIACQVNAQRKIQEILTYVKOHQOQAKLOSPPQSRK 586  
 RESULT 8  
 ABG21963  
 ID ABG21963 standard; Protein; 619 AA.  
 AC  
 XX ABG21963;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #21954.  
 XX  
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 XX  
 PE 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 PI  
 DR WPI: 2001-639362/73.  
 DR N-PSDB: AAS86150.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX  
 PS Claim 20; SEQ ID NO 52322; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 619 AA;  
 XX  
 Query Match 25.7%; Score 149; DB 22; Length 619;  
 Best Local Similarity 100.0%; Pred. No. 5e-143;  
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 STEEGTSACKSTILEIMKREADIKFTEIPKTLANNVGLICKEGRNKKIEODTD 307  
 DB 288 STEEGTSACKSTILEIMKREADIKFTEIPKTLANNVGLICKEGRNKKIEODTD 347  
 QY 308 TKTITSPLOELTYLPNERTITVKGNETCAKAEKEEIMKKTRESYENDIASNNLOAHLLPG 367  
 DB 348 TKTITSPLOELTYLPNERTITVKGNETCAKAEKEEIMKKTRESYENDIASNNLOAHLLPG 407  
 QY 368 LNLNAGLFPPPTSGMPPTSGPPSAMPP 396  
 DB 408 LNLNAGLFPPPTSGMPPTSGPPSAMPP 436

RESULT 9  
 ABG21962 ID ABG21962 standard; Protein; 148 AA.  
 XX  
 AC ABG21962;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #21953.  
 XX  
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PE 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 DR WPI: 2001-639362/73.  
 DR N-PSDB: AAS86149.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 XX  
 PS Claim 20; SEQ ID No 52321; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (II) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.

XX  
 SQ Sequence 148 AA;  
 Query Match 17.1%; Score 99; DB 22; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-92;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 FIPALSVGAIGKGGQHIKQLSRFAGASIKIAPAEAPDAKVRMYITGPPPAQFKAQRI 470  
 DB 11 FIPALSVGAIGKGGQHIKQLSRFAGASIKIAPAEAPDAKVRMYITGPPPAQFKAQRI 70

QY 471 YGKIKENFVSFKREVKLEAHIRVPSFAGRYIGKGGT 509  
 DB 71 YGKIKENFVSFKREVKLEAHIRVPSFAGRYIGKGGT 109

RESULT 10  
 AAM78238 ID AAM78238 standard; Protein; 93 AA.  
 XX  
 AC AAM78238;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38544.  
 XX  
 KW Human: bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157276-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PE 30-JAN-2001; 2001WO-US00668.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI: 2001-488900/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4; SEQ ID NO: 38544; 658bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.  
 XX  
 SQ Sequence 93 AA;  
 Query Match 16.1%; Score 93; DB 22; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-86;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 ALDKINGPOLNFTLTKVAVIPDEMAAQNPLOQPRGRRCIGRGSSRGSGSVSKQPC 194  
 DB 1 ALDKINGPOLNFTLTKVAVIPDEMAAQNPLOQPRGRRCIGRGSSRGSGSVSKQPC 60

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Page 8

OY	195	DLEPLRLVPTQFVGAIIGKEGATIRNITRKOTOS	227
Db	61	DLEPLRLVPTQFVGAIIGKEGATIRNITRKOTOS	93
RESULT 11			
ID	AAM38501	standard; Protein: 93 AA.	
AC	AAM38501;		
XX			
DT	17-OCT-2001	(first entry)	
XX			
DE	Peptide #12538 encoded by probe for measuring placental gene expression.		
XX			
KM	Probe: microarray; human; placenta; antenatal diagnosis;		
RW	genetic disorder.		
XX			
OS	Homo sapiens.		
PD	WC0200157272-A2.		
PJ			
PF	09-AUG-2001.		
XX			
PE	30-JAN-2001; 2001WO-US00663.		
XX			
PR	04-FEB-2000; 2000US-0180312.		
PR	26-MAY-2000; 2000US-0207456.		
PR	30-JUN-2000; 2000US-0608408.		
PR	03-AUG-2000; 2000US-0632366.		
PR	21-SEP-2000; 2000US-0234687.		
PR	27-SEP-2000; 2000US-0236359.		
PR	04-OCT-2000; 2000GB-0024263.		
XX			
PA	(MOLE-) MOLECULAR DYNAMICS INC.		
XI	Penn SG, Hanzel DK, Chen W, Rank DR:		
XX			
DX	WER; 2001-488897/53.		
XX			
PT	human genome-derived single exon nucleic acid probes useful for		
XX	analyzing gene expression in human Placenta -		
PS	Claim 27; SEQ ID NO 38770; 654bp; English.		
CC	The present invention relates to single exon nucleic acid probes (SENP: see A013135-AA157545). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.		
XX			
SQ	Sequence 93 AA:		
Query Match	16.1%; Score 93; DB 22; length 93;		
Best Local Similarity	100.0%; Pred. No. 1.5e-86;		
Matches	93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	135	ALDKLGFGLFEFTLTAKAAYIPDDEMAAOQNPLQOPGRGRGLGGSGSSRGSPGVSKOKPC	194
Db	1	ALDKLGFGLFEFTLTAKAAYIPDDEMAAOQNPLQOPGRGRGRGLGGSGSSRGSPGVSKOKPC	194
OY	195	DLEPLRLVPTQFVGAIIGKEGATIRNITRKOTOS	227
Db	61	DLEPLRLVPTQFVGAIIGKEGATIRNITRKOTOS	93
RESULT 12			
ID	ABG12592	standard; Protein: 583 AA.	
XX			
AC	ABG12592;		
XX			

DT	18-FEB-2002	(first entry)
DE	Novel human diagnostic protein #12583.	
KW	Human: chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder.	
XX		
OS	Homo sapiens.	
PN	MO200175067-A2.	
PD	11-OCT-2001.	
PF	30-MAR-2001; 2001WO-US08631.	
PR	31-MAR-2000; 2000US-0540217.	
XX	23-AUG-2000; 2000US-0649167.	
XX	(HYSE-) HYSEQ INC.	
PI	Dmanac RT, Liu C, Tang YT;	
DR	WPI: 2001-639362/73.	
XX	N-PSDB; AAS76779.	
XX		
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsibilities for genetic disorders or other traits and to assess	
PT	biodiversity -	
XX		
XX	Claim 20: SEQ ID NO 42951; 103bp; English.	
CC	The invention relates to isolated polynucleotide (I) and	
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC	and gene mapping, and in recombinant production of (II). The	
CC	polynucleotides are also used in diagnostics as expressed sequence tags	
CC	for identifying expressed genes. (I) is useful in gene therapy techniques	
CC	to restore normal activity of (II) or to treat disease by	
CC	quantifying a polypeptide (II) binding against it, detecting and as	
CC	diagnostic supplements, (I) is binding partners are useful in medical	
CC	disorders. Involving aberrant protein expression or biological activity.	
CC	The polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABC00010-ABC30377 represent novel human	
CC	diagnostic amino acid sequences of the invention.	
CC	Note: The sequence data for this patent did not appear in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
XX	Sequence 583 AA:	
XX		
XX	Query Match 11.2%: Score 65; DB 22; Length 583;	
XX	Best Local Similarity 100.0%: Pred. No. 35-57;	
XX	Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	200 LVPVPOFGAIGEGGATIRNITKOTOSKIDVHHRKNAAGAEKSTIIILSTPEGTSAACKS 259	
DB	204 LVPVPOFGAIGEGGATIRNITKOTOSKIDVHHRKNAAGAEKSTIIILSTPEGTSAACKS 263	
QY	260 ILEIM 264	
DB	264 ILEIM 268	
XX		
XX	RESULT 13	
XX	ABBA3427 standard; Peptide; 45 AA.	

```

AC  ABB43427;
XX
PD  04-FEB-2002 (first entry)
DE  Peptide #10933 encoded by human foetal liver single exon probe.
XX
KW  Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS  Homo sapiens.
XX
PN  WO200157277-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US00669.
XX
PR  04-FEB-2000; 2000US-0180312.
XX
PR  26-MAY-2000; 2000US-0207456.
XX
PR  30-JUN-2000; 2000US-0608408.
XX
PR  03-AUG-2000; 2000US-0632366.
XX
PR  21-SEP-2000; 2000US-0234687.
XX
PR  27-SEP-2000; 2000US-0236359.
XX
PR  04-OCT-2000; 2000GB-0024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-483447/52.
XX
PT  Human genome-derived single exon nucleic acid probes useful for
XX
PT  analyzing gene expression in human fetal liver -
XX
PS  Claim 27; SEQ ID NO 36062; 639pp + sequence listing; English.
XX
XX
CC  The invention relates to a single exon nucleic acid probe for
CC  measuring human gene expression in a sample derived from human foetal
CC  liver. The single exon nucleic acid probes may be used for predicting,
CC  measuring and displaying gene expression in samples derived from human
CC  fetal liver. The present sequence is a peptide encoded by a single exon
CC  nucleic acid probe of the invention.
CC  Note: The sequence data for this patent did not form part of the
CC  printed specification, but was obtained in electronic format directly
CC  from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 45 AA;

Query Match 7.8%; Score 45; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  315 LOELTLNPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 359
DB  1 LOELTLNPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 45

RESULT 14
ID  AAM64356
ID  AAM64356 standard; Protein; 45 AA.
XX
AC  AAM64356;
XX
DT  05-NOV-2001 (first entry)
XX
DE  Human brain expressed single exon probe encoded protein SEQ ID NO: 36461.
XX
KW  Human; brain expressed exon; gene expression analysis; probe;
XX  microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX  epilepsy; cancer.
XX
OS  Homo sapiens.
XX
PN  WO200157275-A2.

```

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XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US00667.
XX
PR  04-FEB-2000; 2000US-0180312.
XX
PR  26-MAY-2000; 2000US-0207456.
XX
PR  30-JUN-2000; 2000US-0608408.
XX
PR  03-AUG-2000; 2000US-0632366.
XX
PR  21-SEP-2000; 2000US-0234687.
XX
PR  27-SEP-2000; 2000US-0236359.
XX
PR  04-OCT-2000; 2000GB-0024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-483446/52.
XX
PT  Single exon nucleic acid probes for analyzing gene expression in human
XX  brains -
XX
PS  Example 4; SEQ ID NO: 36461; 650pp + Sequence listing; English.
XX
XX
CC  The present invention provides a number of single exon nucleic acid
CC  probes which are derived from genomic sequences expressed in the human
CC  brain. They can be used to measure gene expression in brain cell samples,
CC  which may enable the diagnosis and improved treatment of nervous system
CC  diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC  epilepsy and cancers. The present sequence is a protein encoded by one of
CC  the probes of the invention.
XX
SQ  Sequence 45 AA;

Query Match 7.8%; Score 45; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  315 LOELTLNPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 359
DB  1 LOELTLNPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 45

RESULT 15
ID  AAM37315
ID  AAM37315 standard; Protein; 45 AA.
XX
AC  AAM37315;
XX
DT  17-OCT-2001 (first entry)
XX
DE  Peptide #11352 encoded by probe for measuring placental gene expression.
XX
KW  Probe; microarray; human; placenta; antenatal diagnosis;
XX  genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200157272-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US00663.
XX
PR  04-FEB-2000; 2000US-0180312.
XX
PR  26-MAY-2000; 2000US-0207456.
XX
PR  30-JUN-2000; 2000US-0608408.
XX
PR  03-AUG-2000; 2000US-0632366.
XX
PR  21-SEP-2000; 2000US-0234687.
XX
PR  27-SEP-2000; 2000US-0236359.
XX
PR  04-OCT-2000; 2000GB-0024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.

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us-09-897-778-176.Oligo.rag

Page 10

```
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-48897/53.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX Claim 27: SEQ ID No 37584; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
XX see AA131315-AA157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders.
XX
XX Sequence 45 AA:
SQ
Query Match 7.8%; Score 45; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 315 LOELTYNPERTITVKGNETCAKAEIEIMKKITRESEYENDIASMN 359
DB 1 LOELTYNPERTITVKGNETCAKAEIEIMKKITRESEYENDIASMN 45
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Search completed: April 16, 2003, 16:34:35  
Job time : 134.103 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:12:15 : Search time 40.8818 Seconds  
(without alignments)  
416.711 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579

Sequence: 1 MNKLYIGNSEMAPSDLES.....VKHQOQKALSGPQSRK 579

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents-AI.\*  
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5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backlist1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	579	100.0	579	US-09-643-597-176	Sequence 176, App
2	377	65.1	579	US-09-643-597-348	Sequence 348, App
3	48	8.3	48	US-09-261-855-24	Sequence 24, Appl
4	47	8.1	47	US-09-261-855-23	Sequence 23, Appl
5	42	7.3	49	US-09-261-855-22	Sequence 22, Appl
6	36	6.2	47	US-09-261-855-17	Sequence 17, Appl
7	36	6.2	577	US-09-261-855-2	Sequence 2, Appl
8	32	5.5	47	US-09-261-855-21	Sequence 21, Appl
9	31	3.6	49	US-09-261-855-18	Sequence 18, Appl
10	19	3.3	48	US-09-261-855-20	Sequence 20, Appl
11	14	2.4	14	US-09-261-855-4	Sequence 4, Appl
12	11	1.9	11	US-09-261-855-11	Sequence 11, Appl
13	11	1.9	11	US-09-261-855-14	Sequence 14, Appl
14	11	1.9	11	US-09-261-855-19	Sequence 19, Appl
15	8	1.4	47	US-09-261-855-10	Sequence 10, Appl
16	8	1.4	1375	US-08-665-259-26	Sequence 26, Appl
17	8	1.4	1375	US-08-665-259-26	Sequence 26, Appl
18	8	1.4	1457	US-08-665-259-27	Sequence 27, Appl
19	8	1.4	1457	US-08-665-259-27	Sequence 27, Appl
20	8	1.4	1684	US-08-665-259-25	Sequence 25, Appl
21	8	1.4	1684	US-08-665-259-25	Sequence 25, Appl
22	8	1.4	1704	US-08-762-500-75	Sequence 75, Appl
23	8	1.4	9	US-08-340-283-11	Sequence 11, Appl
24	7	1.2	35	US-08-722-015A-224	Sequence 224, Appl
25	7	1.2	30	US-09-261-855-25	Sequence 25, Appl
26	7	1.2	67	US-08-988-856B-17	Sequence 17, Appl
27	7	1.2	74	US-08-469-260A-498	Sequence 498, App

28	7	1.2	168	US-08-612-788-27	Sequence 27, Appl
29	7	1.2	168	US-09-056-028-27	Sequence 27, Appl
30	7	1.2	181	US-09-134-001C-4852	Sequence 4852, Ap
31	7	1.2	250	US-08-612-788-32	Sequence 32, Appl
32	7	1.2	250	US-09-066-028-32	Sequence 32, Appl
33	7	1.2	299	US-08-879-098-2	Sequence 2, Appl
34	7	1.2	299	US-09-631-548-2	Sequence 2, Appl
35	7	1.2	312	US-09-134-001C-3668	Sequence 3668, Ap
36	7	1.2	339	US-08-248-629A-5	Sequence 5, Appl
37	7	1.2	339	US-08-451-932-5	Sequence 5, Appl
38	7	1.2	339	US-08-452-260-5	Sequence 5, Appl
39	7	1.2	339	US-08-326-788-5	Sequence 5, Appl
40	7	1.2	339	US-08-612-788-5	Sequence 5, Appl
41	7	1.2	339	US-08-605-598B-5	Sequence 5, Appl
42	7	1.2	339	US-08-429-743-5	Sequence 5, Appl
43	7	1.2	339	US-08-866-735-5	Sequence 5, Appl
44	7	1.2	339	US-09-066-028-5	Sequence 5, Appl
45	7	1.2	339	PCT-US95-05107-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-643-597-176  
Sequence 176, Application US/09643597  
Patent No. 6426072  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Lidun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Ranger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Yashir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-176

Query Match 100.0%; Score 579; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKLYIGNSEMAPSDLESIFPKDAKIPYSGFLVKTGYAAVDDPDSMAKIAEASCK	60
DB	1	MNKLYIGNSEMAPSDLESIFPKDAKIPYSGFLVKTGYAAVDDPDSMAKIAEASCK	60
QY	61	IELHGKIEVEHVSPPRORIRKQIRNIPPHQWELVDSLLVOYGVSECEQVNTSE7A	120
DB	61	IELHGKIEVEHVSPPRORIRKQIRNIPPHQWELVDSLLVOYGVSECEQVNTSE7A	120
QY	121	VVNTYSSKQAOALDKINGFQLENTFKAVYIPDEMAAQNPLQOPRGRIQGGSS	180
DB	121	VVNTYSSKQAOALDKINGFQLENTFKAVYIPDEMAAQNPLQOPRGRIQGGSS	180
QY	181	ROGSPGVSQKQCDLPFLVPTQPGVAGIIGKEATIRNTTKQTSKIDVHKENAGA	240
DB	181	ROGSPGVSQKQCDLPFLVPTQPGVAGIIGKEATIRNTTKQTSKIDVHKENAGA	240
QY	241	EKSITLSTPEGTSAACKSILEIMHREKODIKFTEETIPLKILAHNVEGLIGKEGRNKK	

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us-09-897-778-176.Oligo.ra1

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Db 241 EKSTIIISTPEGTSAAKSIILEIMHKEADODIKFTEELPLKILANNFVGRILGEGRNK 300
QY 301 KIEDDTFKITISPLQELTLNPERTITVKGNETCAKAEELMKKIRESEYENDIASMNL 360
Db 301 KIEDDTFKITISPLQELTLNPERTITVKGNETCAKAEELMKKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSANTPEYPOFROSETETVHOIFALSVGAI 420
Db 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSANTPEYPOFROSETETVHOIFALSVGAI 420
QY 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPEAOFKAGRIYGIKEENFV 480
Db 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPEAOFKAGRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSAEVVPBDOTPDENDOVVYKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSAEVVPBDOTPDENDOVVYKIT 540
QY 541 GHFYACOVAORRKIOELITOVKHOQKALQSGPPQSRK 579
Db 541 GHFYACOVAORRKIOELITOVKHOQKALQSGPPQSRK 579
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RESULT 2
US-09-643-597-348
Sequence 348, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
NUMBER OF SEQ ID NOS: 369
CURRENT FILING DATE: 2000-08-21
SOFTWARE: Fasteq for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-348
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Query Match
Best Local Similarity 98.78; Score 377; DB 4; Length 579;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNLTLYGNLSMAAPSDLESIFPKDAKIPYSGPVLKCYAPVNCDEPSAKAIATIASG 60
Db 1 MNLTLYGNLSMAAPSDLESIFPKDAKIPYSGPVLKCYAPVNCDEPSAKAIATIASG 60
QY 61 IELHGKPILEVHSPKRRIRKIOINIPHIOWEVLDLLVYGVESCEQVMTSETA 120
Db 61 IELHGKPILEVHSPKRRIRKIOINIPHIOWEVLDLLVYGVESCEQVMTSETA 120
QY 121 VVWVYSKDOARQALDKLNGFQLENFTLKVAYIPDEMAQONPLQOPRGRLGQSS 160
Db 121 VVWVYSKDOARQALDKLNGFQLENFTLKVAYIPDEMAQONPLQOPRGRLGQSS 160
QY 181 ROGSPGSVKOKPDLPLRLIVPTQFVGALIGKEGATIRNTQOTSKIDVHRKMGAA 240
Db 181 ROGSPGSVKOKPDLPLRLIVPTQFVGALIGKEGATIRNTQOTSKIDVHRKMGAA 240
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QY 241 EKSTIIISTPEGTSAAKSIILEIMHKEADODIKFTEELPLKILANNFVGRILGEGRNK 300
Db 241 EKSTIIISTPEGTSAAKSIILEIMHKEADODIKFTEELPLKILANNFVGRILGEGRNK 300
QY 301 KIEDDTFKITISPLQELTLNPERTITVKGNETCAKAEELMKKIRESEYENDIASMNL 360
Db 301 KIEDDTFKITISPLQELTLNPERTITVKGNETCAKAEELMKKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSANTPEYPOFROSETETVHOIFALSVGAI 420
Db 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSANTPEYPOFROSETETVHOIFALSVGAI 420
QY 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPEAOFKAGRIYGIKEENFV 480
Db 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPEAOFKAGRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSAEVVPBDOTPDENDOVVYKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSAEVVPBDOTPDENDOVVYKIT 540
QY 541 GHFYACOVAORRKIOELITOVKHOQKALQSGPPQSRK 579
Db 541 GHFYACOVAORRKIOELITOVKHOQKALQSGPPQSRK 579
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RESULT 3
US-09-261-855-24
Sequence 24, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 24
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-24
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Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 48;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 492 IRVPSFAAGRVIGKGTYNELONLSAEVVPBDOTPDENDOVVYKIT 539
Db 1 IRVPSFAAGRVIGKGTYNELONLSAEVVPBDOTPDENDOVVYKIT 48
RESULT 4
US-09-261-855-23
Sequence 23, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 23
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-23
Query Match
8.18; Score 47; DB 4; Length 47;
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RESULT 10
US-09-261-855-20
; Sequence 20, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-261-855-20

Query Match
Best Local Similarity 3.3%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 AAGRVIGKRGKTYNELNL 516
DB 7 AAGRVIGKRGKTYNELNL 25

RESULT 11
US-09-261-855-4
; Sequence 4, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-261-855-4

Query Match
Best Local Similarity 2.4%; Score 14; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 6; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GRRGLGORGSSROG 183
DB 1 GRRGLGORGSSROG 14

RESULT 12
US-09-261-855-11
; Sequence 11, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-261-855-11

Query Match
Best Local Similarity 1.9%; Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 HLOMEVLDL 101
DB 1 HLOMEVLDL 11

RESULT 13
US-09-261-855-14
; Sequence 14, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-261-855-14

Query Match
Best Local Similarity 1.9%; Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 TISPLQELTLY 321
DB 1 TISPLQELTLY 11

RESULT 14
US-09-261-855-19
; Sequence 19, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 19
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-261-855-19

Query Match
Best Local Similarity 1.9%; Score 11; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 GQHIKQLSRFA 435
DB 16 GQHIKQLSRFA 26

RESULT 15
US-09-261-855-10
; Sequence 10, Application US/09261855A
; Patent No. 6255055

```

; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE  
; FILE REFERENCE: 960296.95131  
; CURRENT APPLICATION NUMBER: US/09/261,855A  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-261-855-10

Query Match 1.4%; Score 8; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 94 WEVLDSSL 101  
|||||||  
DB 4 WEVLDSSL 11

Search completed: April 16, 2003, 16:38:10  
Job time : 42.8818 secs

1 -

1 -

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:36:47 ; Search time 66.5517 Seconds  
(without alignments)  
657.841 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579

Sequence: 1 MNKLYGNLSNAPSDLES.....VKHOQOKALSGPPSSRRK 579

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 288829 segs, 75613885 residues

Word size: 0

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCR\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	100.0	579	10 US-09-735-705-176	Sequence 176, App
2	579	100.0	579	10 US-09-850-716A-176	Sequence 176, App
3	579	100.0	579	10 US-09-897-778-176	Sequence 176, App
4	377	65.1	579	10 US-09-735-705-348	Sequence 348, App
5	377	65.1	579	10 US-09-850-716A-348	Sequence 348, App
6	377	65.1	579	10 US-09-897-778-348	Sequence 348, App
7	377	65.1	579	10 US-09-897-778-446	Sequence 446, App
8	377	65.1	579	10 US-09-897-778-449	Sequence 449, App
9	376	64.9	586	10 US-09-850-716A-427	Sequence 427, App
10	376	64.9	586	10 US-09-897-778-427	Sequence 427, App
11	93	16.1	93	10 US-09-864-761-48606	Sequence 48606, A
12	48	8.3	48	10 US-09-873-637-24	Sequence 24, Appl
13	47	8.1	47	10 US-09-873-637-23	Sequence 23, Appl
14	45	7.8	45	10 US-09-864-761-45987	Sequence 45987, A
15	42	7.3	49	10 US-09-873-637-22	Sequence 22, Appl
16	36	6.2	47	10 US-09-873-637-17	Sequence 17, Appl
17	36	6.2	577	10 US-09-873-637-2	Sequence 2, Appl
18	32	5.5	47	10 US-09-873-637-21	Sequence 21, Appl
19	24	4.1	261	10 US-09-764-864-1114	Sequence 1114, App

20	21	3.6	49	10 US-09-873-637-18	Sequence 18, Appl
21	20	3.5	20	10 US-09-735-705-397	Sequence 397, App
22	20	3.5	20	10 US-09-735-705-398	Sequence 398, App
23	20	3.5	20	10 US-09-735-705-399	Sequence 399, App
24	20	3.5	20	10 US-09-735-705-400	Sequence 400, App
25	20	3.5	20	10 US-09-735-705-401	Sequence 401, App
26	20	3.5	20	10 US-09-735-705-402	Sequence 402, App
27	20	3.5	20	10 US-09-735-705-403	Sequence 403, App
28	20	3.5	20	10 US-09-735-705-404	Sequence 404, App
29	20	3.5	20	10 US-09-735-705-405	Sequence 405, App
30	20	3.5	20	10 US-09-735-705-406	Sequence 406, App
31	20	3.5	20	10 US-09-735-705-409	Sequence 409, App
32	20	3.5	20	10 US-09-735-705-410	Sequence 410, App
33	20	3.5	20	10 US-09-735-705-411	Sequence 411, App
34	20	3.5	20	10 US-09-735-705-412	Sequence 412, App
35	20	3.5	20	10 US-09-735-705-413	Sequence 413, App
36	20	3.5	20	10 US-09-735-705-414	Sequence 414, App
37	20	3.5	20	10 US-09-735-705-415	Sequence 415, App
38	20	3.5	20	10 US-09-735-705-416	Sequence 416, App
39	20	3.5	20	10 US-09-735-705-417	Sequence 417, App
40	20	3.5	20	10 US-09-735-705-418	Sequence 418, App
41	20	3.5	20	10 US-09-735-705-419	Sequence 419, App
42	20	3.5	20	10 US-09-850-716A-397	Sequence 397, App
43	20	3.5	20	10 US-09-850-716A-398	Sequence 398, App
44	20	3.5	20	10 US-09-850-716A-399	Sequence 399, App
45	20	3.5	20	10 US-09-850-716A-400	Sequence 400, App

## ALIGNMENTS

RESULT 1  
US-09-735-705-176  
Sequence 176, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-176  
Query Match 100.0%; Score 579; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYGNLSNAPSDLESIFRDKKIPVSGFLVKTGYARVDDPDSMALKATELSCK 60  
DB 1 MNKLYGNLSNAPSDLESIFRDKKIPVSGFLVKTGYARVDDPDSMALKATELSCK 60  
OY 61 IELHGKPIEVESHVPRKRIKQIKRINIPHLQWELVDSLIVQYGVESCEQVNTDSETA 120  
DB 61 IELHGKPIEVESHVPRKRIKQIKRINIPHLQWELVDSLIVQYGVESCEQVNTDSETA 120

QY	121	VYVWYYSKKQDAQALDKRNFQENFJENLTUKVYIPDEMAAOQNLODPGRRGIGGOGSS	180
QY	121	VYVWYYSKKQDAQALDKRNFQENFJENLTUKVYIPDEMAAOQNLODPGRRGIGGOGSS	180
Db	121	VYVWYYSKKQDAQALDKRNFQENFJENLTUKVYIPDEMAAOQNLODPGRRGIGGOGSS	180
QY	181	RGSGSGVSKQKRCDPRLILVYPOFGALIGKBGATIRNTJOTQSKIDVHRKKNNGAA	240
Db	181	RGSGSGVSKQKRCDPRLILVYPOFGALIGKBGATIRNTJOTQSKIDVHRKKNNGAA	240
QY	241	EXSTILSTPEGGSAAKSIETIHKRAODIKFETPELTKILAHNNVGRLLGKGRNK	300
Db	241	EXSTILSTPEGGSAAKSIETIHKRAODIKFETPELTKILAHNNVGRLLGKGRNK	300
QY	301	KLEODTPKTTISPIQELTVNPERPTITYGVNVCAGAEELIKKIRRSYONQASML	360
Db	301	KLEODTPKTTISPIQELTVNPERPTITYGVNVCAGAEELIKKIRRSYONQASML	360
QY	361	QAHLLPGLNLAALGELPPISGMPPTSGPSAMTPPYQFQOSTETEVHQIPLASGAI	420
Db	361	QAHLLPGLNLAALGELPPISGMPPTSGPSAMTPPYQFQOSTETEVHQIPLASGAI	420
QY	421	IKQGOHITKOLSTFRFAGASTKTAPEADBAKVXVITITGPPEAFQKAGRTYKIKENFV	480
Db	421	IKQGOHITKOLSTFRFAGASTKTAPEADBAKVXVITITGPPEAFQKAGRTYKIKENFV	480
QY	481	SPKEEYKLEAHIRVPSFAGRIKGGKTYNLEOMSSAEVYVFRQDTENDQOYVYKIT	540
Db	481	SPKEEYKLEAHIRVPSFAGRIKGGKTYNLEOMSSAEVYVFRQDTENDQOYVYKIT	540
QY	541	GHEFYACOVAAQRKIOETLTVYQHOQOQALOSGPPQSRKK	579
Db	541	GHEFYACOVAAQRKIOETLTVYQHOQOQALOSGPPQSRKK	579

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RESULT 2
US-09-850-716A-176
? Sequence 176, Application US/09850716A
? Patent No. US20020115139A1
? GENERAL INFORMATION:
? APPLICANT: Kalos, Michael D.
? APPLICANT: McNeill, Patricia D.
? APPLICANT: Retter, Marc W.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? FILE REFERENCE: 210121.455615
? CURRENT APPLICATION NUMBER: US/09/850.716A
? CURRENT FILING DATE: 2001-05-07
? NUMBER OF SEQ ID NOS: 440
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 176
? LENGTH: 579
? TYPE: prt
? ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match      100.0%; Score 579; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNKLKIGLMSNAPSDLESIFDKAKIFVSPFLVKGYAFVDCPPDESALKATEALSQ 60
Db      . 1 MNKLKIGLMSNAPSDLESIFDKAKIFVSPFLVKGYAFVDCPPDESALKATEALSQ 60

QY      61 IELHCKPIEVESHVSPKKRORIRKIQIRINPPIHLOMEVYDLSLVOYGVESCEQVNTDSEYA 120
Db      . 1 IELHCKPIEVESHVSPKKRORIRKIQIRINPPIHLOMEVYDLSLVOYGVESCEQVNTDSEYA 120

QY      121 VVNVVYSSKKDARQALDKLNGQLENFTLKLVAAYIPDEMAAOQNPLODQPRGRGGIGQGGSS 180
Db      . 121 VVNVVYSSKKDARQALDKLNGQLENFTLKLVAAYIPDEMAAOQNPLODQPRGRGGIGQGGSS 180

QY      181 RGSGSGVSKOKPCDDPLRLRLVPTQFVAALIGKEGATIRNINXKOTOSRIDVHRKEMNGAA 240
Db      . 181 RGSGSGVSKOKPCDDPLRLRLVPTQFVAALIGKEGATIRNINXKOTOSRIDVHRKEMNGAA 240

```

Qy	241	EXHITIIISTPEGTSAMCKSILEIMHKEVQDKFTEETPIKTLANNVGLIGKGRMLK	3000
Db	241	ESITIIISTPEGTSAMCKSILEIMHKEVQDKFTEETPIKTLANNVGLIGKGRMLK	3000
Qy	301	KKEODTPIKTIISPLAELLYMPERTTYVGNVETCAKAEIEIMK1RESYENDIASNML	3600
Db	301	KKEODTPIKTIISPLAELLYMPERTTYVGNVETCAKAEIEIMK1RESYENDIASNML	3600
Qy	361	QAMHLPGLNMLALGTPPTSGMPPPTSGPSAMTPPYPOFQESFETVHOQIPALSVCAI	4200
Db	361	QAMHLPGLNMLALGTPPTSGMPPPTSGPSAMTPPYPOFQESFETVHOQIPALSVCAI	4200
Qy	421	IKGQDHIKOLSPRAGASIKIINAPAPDAVVRVITITGPBPAGCKAGGRYKIKIEENFV	4800
Db	421	IKGQDHIKOLSPRAGASIKIINAPAPDAVVRVITITGPBPAGCKAGGRYKIKIEENFV	4800
Qy	481	SKREEVUKLEAIRIRPSPFAGRGYIGKGKTYNELONJSSAEVVYVRDPTPENDQVYVIT	5400
Db	481	SKREEVUKLEAIRIRPSPFAGRGYIGKGKTYNELONJSSAEVVYVRDPTPENDQVYVIT	5400
Qy	541	GHPYACQVAAKRIJDELLITVVKHODQKALDGSPPORRK	579
Db	541	GHPYACQVAAKRIJDELLITVVKHODQKALDGSPPORRK	579

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RESULT 3
US-09-897-778-176
Sequence 176, Application US/0989778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Marnierakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897.778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-176

Query Match      100.0%; Score 579; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYTGNLSENAAPSDLESIFKDAKIPYSGPFLTKTGYAFVDCPDPSWALKAIEALSGK 60
DB 1 MNKLYTGNLSENAAPSDLESIFKDAKIPYSGPFLTKTGYAFVDCPDPSWALKAIEALSGK 60

QY 61 IELHGAPFIEVHSPVKRQRIKRLQIIRNIPPHLQMEVJDSLVLVOYGVESECDQVMTDSEYA 120
DB 61 IELHGAPFIEVHSPVKRQRIKRLQIIRNIPPHLQMEVJDSLVLVOYGVESECDQVMTDSEYA 120

QY 121 VNVVTVSSKDDARQALDKLNGCFQLENFTLLKVAYIPDEMAAQNPLDQPRGRGLGGRSS 180
DB 121 VNVVTVSSKDDARQALDKLNGCFQLENFTLLKVAYIPDEMAAQNPLDQPRGRGLGGRSS 180

QY 181 RQSGPQSVSKQPCDPLRLVPTQFVGAIGKGGATIRNITKQTSKIDVHRKRENGAA 240
DB 181 RQSGPQSVSKQPCDPLRLVPTQFVGAIGKGGATIRNITKQTSKIDVHRKRENGAA 240

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QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPIPLKILAHNNFVGRILGEGRNK 300  
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPIPLKILAHNNFVGRILGEGRNK 300  
QY 301 KIBODTDTKITISPLQELTLNPERTITVKGNETCAKAEIEMKIRRESYENDIASMNL 360  
DB 301 KIBODTDTKITISPLQELTLNPERTITVKGNETCAKAEIEMKIRRESYENDIASMNL 360  
QY 361 QAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEQSETEVHOPIFALSVAL 420  
DB 361 QAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEQSETEVHOPIFALSVAL 420  
QY 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVRWITITGPEPOFAOGRIYGIKEENFV 480  
DB 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVRWITITGPEPOFAOGRIYGIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPDENDDVVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPDENDDVVKIT 540  
QY 541 GHFYACOVAORKIOELITVOKHOQOKALOSGPPSRRK 579  
DB 541 GHFYACOVAORKIOELITVOKHOQOKALOSGPPSRRK 579

## RESULT 4

US-09-735-705-348  
; Sequence 348, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Pan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-348

Query Match 65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALS 60  
DB 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALS 60  
QY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSE 120  
DB 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSE 120  
QY 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRGIGOGSS 180  
DB 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRGIGOGSS 180  
QY 181 ROGSFVSVKORPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGA 240  
DB 181 ROGSFVSVKORPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGA 240

DB 181 ROGSFVSVKORPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGA 240  
QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPIPLKILAHNNFVGRILGEGRNK 300  
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPIPLKILAHNNFVGRILGEGRNK 300  
QY 301 KIBODTDTKITISPLQELTLNPERTITVKGNETCAKAEIEMKIRRESYENDIASMNL 360  
DB 301 KIBODTDTKITISPLQELTLNPERTITVKGNETCAKAEIEMKIRRESYENDIASMNL 360  
QY 361 QAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEQSETEVHOPIFALSVAL 420  
DB 361 QAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEQSETEVHOPIFALSVAL 420  
QY 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVRWITITGPEPOFAOGRIYGIKEENFV 480  
DB 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVRWITITGPEPOFAOGRIYGIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPDENDDVVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPDENDDVVKIT 540  
QY 541 GHFYACOVAORKIOELITVOKHOQOKALOSGPPSRRK 579  
DB 541 GHFYACOVAORKIOELITVOKHOQOKALOSGPPSRRK 579

## RESULT 5

US-09-850-716A-348  
; Sequence 348, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Rafter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-348

Query Match 65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALS 60  
DB 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALS 60  
QY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSE 120  
DB 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSE 120  
QY 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRGIGOGSS 180  
DB 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRGIGOGSS 180  
QY 181 ROGSFVSVKORPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGA 240  
DB 181 ROGSFVSVKORPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGA 240  
QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPIPLKILAHNNFVGRILGEGRNK 300  
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPIPLKILAHNNFVGRILGEGRNK 300  
QY 301 KIBODTDTKITISPLQELTLNPERTITVKGNETCAKAEIEMKIRRESYENDIASMNL 360  
DB 301 KIBODTDTKITISPLQELTLNPERTITVKGNETCAKAEIEMKIRRESYENDIASMNL 360

Db 301 KIEODTDTKITISLQDELTYNPERTIVKGNVETCAKAEELMKKIRSEYNDIASNML 360  
QY 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
Db 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
QY 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYMVIITGPEAOFKAOGRTYKIKENNV 480  
Db 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYMVIITGPEAOFKAOGRTYKIKENNV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQTPDENDOVYAKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQTPDENDOVYAKIT 540  
QY 541 GHFYACQVAKRKIOEILTYVKQHOOQKALOSGPPQSRK 579  
Db 541 GHFYACQVAKRKIOEILTYVKQHOOQKALOSGPPQSRK 579

RESULT 6  
US-09-897-778-348  
Sequence 348, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C16  
CURRENT FILING DATE: 2001-06-28  
CURRENT APPLICATION NUMBER: US/09/897.778  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-348

Query Match 65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLTYGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
Db 1 MNKLTYGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
QY 61 IELHGKPLEVEHSPKROIRKIQIRNIPHLQWEVDLSLVOYGVESCEQVNDSETA 120  
Db 61 IELHGKPLEVEHSPKROIRKIQIRNIPHLQWEVDLSLVOYGVESCEQVNDSETA 120  
QY 121 VVNYTSSKDOARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPRGRGLGGRSS 180  
Db 121 VVNYTSSKDOARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPRGRGLGGRSS 180  
QY 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIKRGATIRNITKQDSKIDVHREMGAA 240  
Db 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIKRGATIRNITKQDSKIDVHREMGAA 240  
QY 241 EKSTIILSTPEGTSACKSILEIMKREKODIKFTEELPKILAHNNFVGRILGEGRNK 300  
Db 241 EKSTIILSTPEGTSACKSILEIMKREKODIKFTEELPKILAHNNFVGRILGEGRNK 300  
QY 301 KIEODTDTKITISLQDELTYNPERTIVKGNVETCAKAEELMKKIRSEYNDIASNML 360  
Db 301 KIEODTDTKITISLQDELTYNPERTIVKGNVETCAKAEELMKKIRSEYNDIASNML 360

Db 301 KIEODTDTKITISLQDELTYNPERTIVKGNVETCAKAEELMKKIRSEYNDIASNML 360  
QY 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
Db 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
QY 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYMVIITGPEAOFKAOGRTYKIKENNV 480  
Db 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYMVIITGPEAOFKAOGRTYKIKENNV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQTPDENDOVYAKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQTPDENDOVYAKIT 540  
QY 541 GHFYACQVAKRKIOEILTYVKQHOOQKALOSGPPQSRK 579  
Db 541 GHFYACQVAKRKIOEILTYVKQHOOQKALOSGPPQSRK 579

RESULT 7  
US-09-897-778-446  
Sequence 446, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C16  
CURRENT FILING DATE: 2001-06-28  
CURRENT APPLICATION NUMBER: US/09/897.778  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 446  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-446

Query Match 65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLTYGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
Db 1 MNKLTYGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
QY 61 IELHGKPLEVEHSPKROIRKIQIRNIPHLQWEVDLSLVOYGVESCEQVNDSETA 120  
Db 61 IELHGKPLEVEHSPKROIRKIQIRNIPHLQWEVDLSLVOYGVESCEQVNDSETA 120  
QY 121 VVNYTSSKDOARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPRGRGLGGRSS 180  
Db 121 VVNYTSSKDOARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPRGRGLGGRSS 180  
QY 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIKRGATIRNITKQDSKIDVHREMGAA 240  
Db 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIKRGATIRNITKQDSKIDVHREMGAA 240  
QY 241 EKSTIILSTPEGTSACKSILEIMKREKODIKFTEELPKILAHNNFVGRILGEGRNK 300  
Db 241 EKSTIILSTPEGTSACKSILEIMKREKODIKFTEELPKILAHNNFVGRILGEGRNK 300  
QY 301 KIEODTDTKITISLQDELTYNPERTIVKGNVETCAKAEELMKKIRSEYNDIASNML 360  
Db 301 KIEODTDTKITISLQDELTYNPERTIVKGNVETCAKAEELMKKIRSEYNDIASNML 360



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QY 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPYPYQFQSEETVHOFIPALSVGAI 420
DB 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPYPYQFQSEETVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMVYITGPPEAOFRAGRIYGIKEENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMVYITGPPEAOFRAGRIYGIKEENFV 480
QY 481 SPEEVLKLAHIRVPSFAAGRVIGKGTVELNLNLSSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPEEVLKLAHIRVPSFAAGRVIGKGTVELNLNLSSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACOVAAORKIOELITVOYKHOQOKALOSGPPSRRK 579
DB 541 GHFYACOVAAORKIOELITVOYKHOQOKALOSGPPSRRK 579

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## RESULT 8

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US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshitiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

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## Query Match

65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MNKIYIGNLSENAPSDLESIFKDAKIPVSGPPLVYTGAFVDCPDSEWALKATIALSGKI 60
DB 1 MNKIYIGNLSENAPSDLESIFKDAKIPVSGPPLVYTGAFVDCPDSEWALKATIALSGKI 60
QY 61 ELHGKPIEVESHVPRKQRIKLIQIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 120
DB 61 ELHGKPIEVESHVPRKQRIKLIQIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 120
QY 121 VVNTYSSKDOARALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGORGSSR 180
DB 121 VVNTYSSKDOARALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGORGSSR 180
QY 181 ROGSPGSVSKOPCDLPLRLVPTQFVGAIIKEGATIRNITKOTOSKIDVHRKENAGAA 240
DB 181 ROGSPGSVSKOPCDLPLRLVPTQFVGAIIKEGATIRNITKOTOSKIDVHRKENAGAA 240
QY 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPIKLIHANNFVRLIGKGRNKK 300
DB 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPIKLIHANNFVRLIGKGRNKK 300
QY 301 KIEODTDTKTIISPLQELITLYNPERITYVGNVETCAKAEELIMKIRRESYENDIASMNL 360
DB 301 KIEODTDTKTIISPLQELITLYNPERITYVGNVETCAKAEELIMKIRRESYENDIASMNL 360

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QY 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPYPYQFQSEETVHOFIPALSVGAI 420
DB 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPYPYQFQSEETVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMVYITGPPEAOFRAGRIYGIKEENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMVYITGPPEAOFRAGRIYGIKEENFV 480
QY 481 SPEEVLKLAHIRVPSFAAGRVIGKGTVELNLNLSSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPEEVLKLAHIRVPSFAAGRVIGKGTVELNLNLSSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACOVAAORKIOELITVOYKHOQOKALOSGPPSRRK 579
DB 541 GHFYACOVAAORKIOELITVOYKHOQOKALOSGPPSRRK 579

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## RESULT 9

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US-09-850-716A-427
; Sequence 427, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kaelos, Michael D.
; APPLICANT: McNell, Patricia D.
; APPLICANT: Reltzer, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-427

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## Query Match

64.9%; Score 376; DB 10; Length 586;  
Best Local Similarity 99.7%; Pred. No. 0;

Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 NKLIYIGNLSENAPSDLESIFKDAKIPVSGPPLVYTGAFVDCPDSEWALKATIALSGKI 61
DB 2 NKLIYIGNLSENAPSDLESIFKDAKIPVSGPPLVYTGAFVDCPDSEWALKATIALSGKI 61
QY 62 ELHGKPIEVESHVPRKQRIKLIQIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 121
DB 62 ELHGKPIEVESHVPRKQRIKLIQIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 121
QY 122 VVNTYSSKDOARALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGORGSSR 181
DB 122 VVNTYSSKDOARALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGORGSSR 181
QY 182 OQSPGSVSKOPCDLPLRLVPTQFVGAIIKEGATIRNITKOTOSKIDVHRKENAGAAE 241
DB 182 OQSPGSVSKOPCDLPLRLVPTQFVGAIIKEGATIRNITKOTOSKIDVHRKENAGAAE 241
QY 242 KSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPIKLIHANNFVRLIGKGRNKK 301
DB 242 KSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPIKLIHANNFVRLIGKGRNKK 301
QY 302 IEODTDTKTIISPLQELITLYNPERITYVGNVETCAKAEELIMKIRRESYENDIASMNLQ 361
DB 302 IEODTDTKTIISPLQELITLYNPERITYVGNVETCAKAEELIMKIRRESYENDIASMNLQ 361
QY 362 AHLIPGLNMLNGLPPTSGMPPTSGPPSAMPYPYQFQSEETVHOFIPALSVGAI 421
DB 362 AHLIPGLNMLNGLPPTSGMPPTSGPPSAMPYPYQFQSEETVHOFIPALSVGAI 421
QY 422 IKGOGHITKOLSRFAGASIKIAPAPADAKVMVYITGPPEAOFRAGRIYGIKEENFV 481
DB 422 IKGOGHITKOLSRFAGASIKIAPAPADAKVMVYITGPPEAOFRAGRIYGIKEENFV 481
QY 481 SPEEVLKLAHIRVPSFAAGRVIGKGTVELNLNLSSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPEEVLKLAHIRVPSFAAGRVIGKGTVELNLNLSSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACOVAAORKIOELITVOYKHOQOKALOSGPPSRRK 579
DB 541 GHFYACOVAAORKIOELITVOYKHOQOKALOSGPPSRRK 579

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Query Match 16.1%; Score 93; DB 10; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.2e-82;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 135 ALDRKNGFQLENTFLKAVIPDEMAAQNPLQOPGRGRGLGCRGSSRSGSPSSVSKORFC 194
Db 1 ALDKNGFQLENTFLKAVIPDEMAAQNPLQOPGRGRGLGCRGSSRSGSPSSVSKORFC 60

Oy 195 DLPLRLVPTQFVGAIIKREGATINNTKOTOS 227
Db 61 DLPLRLVPTQFVGAIIKREGATINNTKOTOS 93

RESULT 12
US-09-873-637-24
; Sequence 24, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873.637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-637-24

Query Match 8.3%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.4e-39;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 492 IRVPSFAAGRYIGKGTIVNELQNLSSAEVVPVRDQTPDENDQVVKI 539
Db 1 IRVPSFAAGRYIGKGTIVNELQNLSSAEVVPVRDQTPDENDQVVKI 48

RESULT 13
US-09-873-637-23
; Sequence 23, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873.637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-637-23

Query Match 8.1%; Score 47; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 6.7e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 410 QFTRALSGAIIIGKGGHIIKQLSRFAGASIKIAPAEAPDAKVRMYII 456
Db 1 QFTRALSGAIIIGKGGHIIKQLSRFAGASIKIAPAEAPDAKVRMYII 47

RESULT 14
US-09-864-761-45987
; Sequence 45987, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864.761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180.312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207.456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632.366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236.359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234.687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608.408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774.203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45987
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021876.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: P78004, EVALUE 2.80e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA427803.1, EVALUE 9.00e-19
US-09-864-761-45987

Query Match 7.8%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.5e-36;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 315 LOELTYNPERITIVKGNVETCAKAEELMKIRSYENDIASMN 359
Db 1 LOELTYNPERITIVKGNVETCAKAEELMKIRSYENDIASMN 45

RESULT 15
US-09-873-637-22
; Sequence 22, Application US/09873637
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Thu Apr 17 07:55:17 2003

us-09-897-778-176.Oligo.rapb

Page 8

Patent No. US20020061543A1  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/873,637  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 49  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-873-637-22

Query Match 7.3%; Score 42; DB 10; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 8 VGRLLGEGGRNLKITEODTDRKITISPLQELTYNPERITV 49

Search completed: April 16, 2003, 16:48:41  
Job time: 67.5517 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:34:47 ; Search time 392.655 Seconds  
(without alignments)  
950.708 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579

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- 25: /cgn2\_6/ptodata/1/paa/US102.COMB.pep.\*
- 26: /cgn2\_6/ptodata/1/paa/US103.COMB.pep.\*
- 27: /cgn2\_6/ptodata/1/paa/US60.COMB.pep.\*

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# SUMMARIES

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2	579	100.0	579	18	US-09-466-396A-176
3	579	100.0	579	18	US-09-476-496A-176
4	579	100.0	579	18	US-09-480-884A-176
5	579	100.0	579	19	US-09-510-376A-176
6	579	100.0	579	19	US-09-542-615A-176

7	579	100.0	579	20	US-09-606-421A-176	Sequence 176, App
8	579	100.0	579	20	US-09-606-421B-176	Sequence 176, App
9	579	100.0	579	20	US-09-630-940A-176	Sequence 176, App
10	579	100.0	579	20	US-09-630-940B-176	Sequence 176, App
11	579	100.0	579	20	US-09-662-786-176	Sequence 176, App
12	579	100.0	579	20	US-09-685-696-176	Sequence 176, App
13	579	100.0	579	21	US-09-735-705-176	Sequence 176, App
14	579	100.0	579	21	US-09-791-537-49019	Sequence 49019, A
15	579	100.0	579	22	US-09-850-716-176	Sequence 176, App
16	579	100.0	579	22	US-09-850-716A-176	Sequence 176, App
17	579	100.0	579	22	US-09-897-778-176	Sequence 176, App
18	579	100.0	579	24	US-10-007-700-176	Sequence 176, App
19	579	100.0	579	25	US-10-117-982-176	Sequence 176, App
20	478	82.6	579	25	US-09-791-537-86130	Sequence 86130, A
21	398	68.7	579	25	US-10-117-982-484	Sequence 484, App
22	377	65.1	579	1	PCT-US01-47576-348	Sequence 348, App
23	377	65.1	579	1	PCT-US01-47576-446	Sequence 446, App
24	377	65.1	579	19	PCT-US01-47576-449	Sequence 449, App
25	377	65.1	579	20	US-09-606-421A-348	Sequence 348, App
26	377	65.1	579	20	US-09-606-421B-348	Sequence 348, App
27	377	65.1	579	20	US-09-630-940A-348	Sequence 348, App
28	377	65.1	579	20	US-09-630-940B-348	Sequence 348, App
29	377	65.1	579	20	US-09-662-786-348	Sequence 348, App
30	377	65.1	579	20	US-09-685-696-348	Sequence 348, App
31	377	65.1	579	21	US-09-735-705-348	Sequence 348, App
32	377	65.1	579	22	US-09-850-716-348	Sequence 348, App
33	377	65.1	579	22	US-09-850-716A-348	Sequence 348, App
34	377	65.1	579	22	US-09-897-778-348	Sequence 348, App
35	377	65.1	579	22	US-09-897-778-446	Sequence 446, App
36	377	65.1	579	22	US-09-897-778-449	Sequence 449, App
37	377	65.1	579	24	US-10-007-700-348	Sequence 348, App
38	377	65.1	579	24	US-10-007-700-446	Sequence 446, App
39	377	65.1	579	24	US-10-007-700-449	Sequence 449, App
40	377	65.1	579	25	US-10-117-982-348	Sequence 348, App
41	377	65.1	579	25	US-10-117-982-446	Sequence 446, App
42	377	65.1	579	25	US-10-117-982-449	Sequence 449, App
43	377	65.1	579	25	US-10-117-982-484	Sequence 484, App
44	377	65.1	579	25	US-10-117-982-480	Sequence 480, App
45	376	64.9	586	1	PCT-US01-47576-427	Sequence 427, App

## ALIGNMENTS

RESULT 1  
PCT-US01-47576-176  
Sequence 176, Application PC/TUS0147576  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tonglong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Veddyk, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Peckman, David W.  
APPLICANT: Cai, Peng  
APPLICANT: Fay, Teresa M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.45503PC  
CURRENT APPLICATION NUMBER: PCT/US01/47576  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FASTSQ for Windows Version 4.0

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Page 2

SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US01-47576-176

Query Match  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNSENAAAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60  
DB 1 MNKLYIGNSENAAAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60  
OY 61 IELHGKPIEVHVSVKRORIKKQIRNIPPHLOMEVLSLVOYGVESECOVNTDSETA 120  
DB 61 IELHGKPIEVHVSVKRORIKKQIRNIPPHLOMEVLSLVOYGVESECOVNTDSETA 120  
OY 121 VVAVVYSSKQOARQALDKLNGFOLNFTLVKVAIPDEMAAOQNPLOQPRGRGLGGRSS 180  
DB 121 VVAVVYSSKQOARQALDKLNGFOLNFTLVKVAIPDEMAAOQNPLOQPRGRGLGGRSS 180  
OY 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTOSKIDVHKRENAGAA 240  
DB 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTOSKIDVHKRENAGAA 240  
OY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIANNFVGRLLICEGRNLK 300  
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIANNFVGRLLICEGRNLK 300  
OY 301 KIEQDDTKITISPLQELTLVNPERRITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
DB 301 KIEQDDTKITISPLQELTLVNPERRITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
OY 361 QAHLIPGLNLNLSLFPPTSGMPPTSGPPSAMPPTPYQFQSESETETVHOFIPALSVGAI 420  
DB 361 QAHLIPGLNLNLSLFPPTSGMPPTSGPPSAMPPTPYQFQSESETETVHOFIPALSVGAI 420  
OY 421 IGKQGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAKRACGRITGRIKEENFV 480  
DB 421 IGKQGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAKRACGRITGRIKEENFV 480  
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELONLSAEVYVPRDQTPENDQVYVKKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELONLSAEVYVPRDQTPENDQVYVKKIT 540  
OY 541 GHFYACQVAKRKIOEILTVQVQKHOQKALOSGPPSRRK 579  
DB 541 GHFYACQVAKRKIOEILTVQVQKHOQKALOSGPPSRRK 579

RESULT 2  
US-09-466-396A-176  
Sequence 176, Application US/09466396A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.455C4  
CURRENT APPLICATION NUMBER: US/09/466.396A  
CURRENT FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-466-396A-176

Query Match  
Best Local Similarity 100.0%; Score 579; DB 18; Length 579;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNSENAAAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60  
DB 1 MNKLYIGNSENAAAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60  
OY 61 IELHGKPIEVHVSVKRORIKKQIRNIPPHLOMEVLSLVOYGVESECOVNTDSETA 120  
DB 61 IELHGKPIEVHVSVKRORIKKQIRNIPPHLOMEVLSLVOYGVESECOVNTDSETA 120  
OY 121 VVAVVYSSKQOARQALDKLNGFOLNFTLVKVAIPDEMAAOQNPLOQPRGRGLGGRSS 180  
DB 121 VVAVVYSSKQOARQALDKLNGFOLNFTLVKVAIPDEMAAOQNPLOQPRGRGLGGRSS 180  
OY 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTOSKIDVHKRENAGAA 240  
DB 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTOSKIDVHKRENAGAA 240  
OY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIANNFVGRLLICEGRNLK 300  
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIANNFVGRLLICEGRNLK 300  
OY 301 KIEQDDTKITISPLQELTLVNPERRITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
DB 301 KIEQDDTKITISPLQELTLVNPERRITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
OY 361 QAHLIPGLNLNLSLFPPTSGMPPTSGPPSAMPPTPYQFQSESETETVHOFIPALSVGAI 420  
DB 361 QAHLIPGLNLNLSLFPPTSGMPPTSGPPSAMPPTPYQFQSESETETVHOFIPALSVGAI 420  
OY 421 IGKQGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAKRACGRITGRIKEENFV 480  
DB 421 IGKQGHIKOLSRFAGASIKIAPAEAPDAKVRNVIITGPPEAKRACGRITGRIKEENFV 480  
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELONLSAEVYVPRDQTPENDQVYVKKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELONLSAEVYVPRDQTPENDQVYVKKIT 540  
OY 541 GHFYACQVAKRKIOEILTVQVQKHOQKALOSGPPSRRK 579  
DB 541 GHFYACQVAKRKIOEILTVQVQKHOQKALOSGPPSRRK 579

RESULT 3  
US-09-476-496A-176  
Sequence 176, Application US/09476496A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF  
FILE REFERENCE: 210121.455C5  
CURRENT APPLICATION NUMBER: US/09/476.496A  
CURRENT FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-476-496A-176

Query Match  
Best Local Similarity 100.0%; Score 579; DB 18; Length 579;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNSENAAAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60  
DB 1 MNKLYIGNSENAAAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60  
OY 61 IELHGKPIEVHVSVKRORIKKQIRNIPPHLOMEVLSLVOYGVESECOVNTDSETA 120  
DB 61 IELHGKPIEVHVSVKRORIKKQIRNIPPHLOMEVLSLVOYGVESECOVNTDSETA 120

```
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAOQNPLQOPGRGRGLGGRSS 180
      |||
Db 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAOQNPLQOPGRGRGLGGRSS 180
QY 181 RQSGSGSVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHRKENAGAA 240
      |||
Db 181 RQSGSGSVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNK 300
      |||
Db 241 EKSTITLSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNK 300
QY 301 KIEODTDRKITISPLQELTYNPERTTVKGNVETCAKAEELMKKIRESENDIASMNL 360
      |||
Db 301 KIEODTDRKITISPLQELTYNPERTTVKGNVETCAKAEELMKKIRESENDIASMNL 360
QY 361 QAHILPGLNMLNGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
      |||
Db 361 QAHILPGLNMLNGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAFKAGRIYGIKEENFV 480
      |||
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAFKAGRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGGKTVNELQNLSSAEVVPDROTDPENDQVVKIT 540
      |||
Db 481 SPKEEVKLEAHIRVPSFAAGRYIGKGGKTVNELQNLSSAEVVPDROTDPENDQVVKIT 540
QY 541 GHFYACOVAORKIOELITQVOKHOQKALQSGPPQSRK 579
      |||
Db 541 GHFYACOVAORKIOELITQVOKHOQKALQSGPPQSRK 579
```

## RESULT 4

```
US-09-480-884A-176
: Sequence 176, Application US/09480884A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C6
: CURRENT APPLICATION NUMBER: US/09/480, 884A
: CURRENT FILING DATE: 2001-08-27
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-480-884A-176
```

```
Query Match 100.0%; Score 579; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60
      |||
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60
QY 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLYGVVSCQVNTDSETA 120
      |||
Db 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLYGVVSCQVNTDSETA 120
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAOQNPLQOPGRGRGLGGRSS 180
      |||
Db 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAOQNPLQOPGRGRGLGGRSS 180
QY 181 RQSGSGSVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHRKENAGAA 240
      |||
```

```
Db 181 RQSGSGSVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHRKENAGAA 240
      |||
QY 241 EKSTITLSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNK 300
      |||
Db 241 EKSTITLSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNK 300
QY 301 KIEODTDRKITISPLQELTYNPERTTVKGNVETCAKAEELMKKIRESENDIASMNL 360
      |||
Db 301 KIEODTDRKITISPLQELTYNPERTTVKGNVETCAKAEELMKKIRESENDIASMNL 360
QY 361 QAHILPGLNMLNGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
      |||
Db 361 QAHILPGLNMLNGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAFKAGRIYGIKEENFV 480
      |||
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAFKAGRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGGKTVNELQNLSSAEVVPDROTDPENDQVVKIT 540
      |||
Db 481 SPKEEVKLEAHIRVPSFAAGRYIGKGGKTVNELQNLSSAEVVPDROTDPENDQVVKIT 540
QY 541 GHFYACOVAORKIOELITQVOKHOQKALQSGPPQSRK 579
      |||
Db 541 GHFYACOVAORKIOELITQVOKHOQKALQSGPPQSRK 579
```

## RESULT 5

```
US-09-510-376A-176
: Sequence 176, Application US/09510376A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C7
: CURRENT APPLICATION NUMBER: US/09/510, 376A
: CURRENT FILING DATE: 2001-08-21
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-510-376A-176
```

```
Query Match 100.0%; Score 579; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60
      |||
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60
QY 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLYGVVSCQVNTDSETA 120
      |||
Db 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLYGVVSCQVNTDSETA 120
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAOQNPLQOPGRGRGLGGRSS 180
      |||
Db 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAOQNPLQOPGRGRGLGGRSS 180
QY 181 RQSGSGSVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHRKENAGAA 240
      |||
Db 181 RQSGSGSVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNK 300
      |||
Db 241 EKSTITLSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNK 300
```

```

QY 301 KIEODTPKRIITISLQJELTYNPERITIVKGVNECAKAEELIMKKIRRESYENDIASMNL 360
QY 301 KIEODTPKRIITISLQJELTYNPERITIVKGVNECAKAEELIMKKIRRESYENDIASMNL 360
Db 301 KIEODTPKRIITISLQJELTYNPERITIVKGVNECAKAEELIMKKIRRESYENDIASMNL 360
QY 361 QAHLLIPGNTLUALFLPPTSGMPPTSGPPSAMTPPYPOEJOSETETVIOEFLPALSVAI 420
Db 361 QAHLLIPGNTLUALFLPPTSGMPPTSGPPSAMTPPYPOEJOSETETVIOEFLPALSVAI 420
QY 421 ICKGQOHIKOLSRFAGASIKIAPAEAPDAKVRMYITIGPEAOFKQGRITAEKIKENFV 480
Db 421 ICKGQOHIKOLSRFAGASIKIAPAEAPDAKVRMYITIGPEAOFKQGRITAEKIKENFV 480
QY 481 SPREEVKLEAHIRVPSFAAGRVIGKGGKTVNELNLSAEVVPVPROGTPDENDDVYKIT 540
Db 481 SPREEVKLEAHIRVPSFAAGRVIGKGGKTVNELNLSAEVVPVPROGTPDENDDVYKIT 540
QY 541 GHFYACQVAKRKIOELITQYKHQOQKALGSPQSRK 579
Db 541 GHFYACQVAKRKIOELITQYKHQOQKALGSPQSRK 579

RESULT 5
US-09-542-615A-176
: Sequence 176. Application US/09542615A
: GENERAL INFORMATION:
: Applicant: Wang, Tonglong
: Applicant: Fan, Liqun
: Applicant: Kalos, Michael D.
: Applicant: Bangur, Chaltanya S.
: Applicant: Hosken, Nancy A.
: Applicant: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.453C8
: CURRENT APPLICATION NUMBER: US/09/542.615A
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-542-615A-176

```

	Query Match	Similarity	100.0%	Score	579;	DB	19;	Length	579;
	Best Local	Similarity	100.0%	Pred. No.	0;				
	Matches	579;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
Qy	1	MKRLTIGNLSENAPSDLESIFKDAKITVSGFVLTKGYAFVAVCCPESMAKKAIEALISGK	60						
Db	1	MKRLTIGNLSENAPSDLESIFKDAKITVSGFVLTKGYAFVAVCCPESMAKKAIEALISGK	60						
Qy	61	IELHCKPIEVEHSVPRKQRIKRIQIRNIPHLQHEVLDLSLYGYGVESCEQVYNDDETA	120						
Db	61	IELHCKPIEVEHSVPRKQRIKRIQIRNIPHLQHEVLDLSLYGYGVESCEQVYNDDETA	120						
Qy	121	VVNVYSSKKDARALDKLNGRLQENFLTKAVYIPDEMAQOMPLQOPGRGGLGQSSS	180						
Db	121	VVNVYSSKKDARALDKLNGRLQENFLTKAVYIPDEMAQOMPLQOPGRGGLGQSSS	180						
Qy	181	RGSGSGSVSRKPCDDPLRLVLPQFVATIGKGCATIRITVQDOSKIDVHKRENGAA	240						
Db	181	RGSGSGSVSRKPCDDPLRLVLPQFVATIGKGCATIRITVQDOSKIDVHKRENGAA	240						
Qy	241	EXSTLTSTPSTGSAAKSLTEIMKKEADQIKFPEELPLKLIANHNFGRLGKEGRNLK	300						
Db	241	EXSTLTSTPSTGSAAKSLTEIMKKEADQIKFPEELPLKLIANHNFGRLGKEGRNLK	300						
Qy	301	KLEQDTPDKITISPLDELTLVNPERTITVYKGNVETCKAKAABELIMKKIRESTENDIASNL	360						
Db	301	KLEQDTPDKITISPLDELTLVNPERTITVYKGNVETCKAKAABELIMKKIRESTENDIASNL	360						

```

QY 361 QAHLLPGLNLAALPLPPTSGMPPSPGSPSMTPPPOFEOSETETVHOQFIPALSGAI 420
Db 361 QAHLLPGLNLAALPLPPTSGMPPSPGSPSMTPPPOFEOSETETVHOQFIPALSGAI 420
QY 421 IKGOGHOKIOLSRFAGASIKIAPAEAPDAKVMYIITGPEPAOFKAGORITGKIKEENFV 480
Db 421 IKGOGHOKIOLSRFAGASIKIAPAEAPDAKVMYIITGPEPAOFKAGORITGKIKEENFV 480
QY 481 SPREEKLEAHIRPSPFAAGRVIGKGGKTVELNLNLSSAEVWVPDRQDPDENDQYVVKIT 540
Db 481 SPREEKLEAHIRPSPFAAGRVIGKGGKTVELNLNLSSAEVWVPDRQDPDENDQYVVKIT 540
QY 541 GHEFYACOVAORRIGIELITQYKHQHQOQALOSGPOSSRRK 579
Db 541 GHEFYACOVAORRIGIELITQYKHQHQOQALOSGPOSSRRK 579

RESULT 7
US-09-606-421A-176
Sequence 176, Application US/09606421A
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606.421A
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 354
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO. 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421A-176

```

Query Match	Similarity	Score	DB	Length
Best Local	100.0%	579	20	579
Matches	579	Conservative	0	Mismatches
			0	Indels
			0	Gaps
QY	1	MMKLIGLNSNAPSDLESIEFKDAKIVPSGPFVLKTVGAFVDCPPESWALKALIEALSGK	60	
Db	1	MMKLIGLNSNAPSDLESIEFKDAKIVPSGPFVLKTVGAFVDCPPESWALKALIEALSGK	60	
QY	61	IELHCKPIEVSHVSPKKRORIARKIOTIRNIPPHIQMEVDSILLYOYGVESCEQVMTDETA	120	
Db	61	IELHCKPIEVSHVSPKKRORIARKIOTIRNIPPHIQMEVDSILLYOYGVESCEQVMTDETA	120	
QY	121	VVNVVYSSKDDARALDKLNGFQLENTFLKVALYIPDEMAQOQNPLOQGRGRGQGGSS	180	
Db	121	VVNVVYSSKDDARALDKLNGFQLENTFLKVALYIPDEMAQOQNPLOQGRGRGQGGSS	180	
QY	181	RGSGBSGSKKPCDDPLRLRLVPTQGVAAIIGKGATIRNTKQTSKIDVHRKENGAA	240	
Db	181	RGSGBSGSKKPCDDPLRLRLVPTQGVAAIIGKGATIRNTKQTSKIDVHRKENGAA	240	
QY	241	EKSITILSPBGTSAAKCSILIEIMKKEADIKFEEELPLKTLAHNNFVGRILGEGRNLK	300	
Db	241	EKSITILSPBGTSAAKCSILIEIMKKEADIKFEEELPLKTLAHNNFVGRILGEGRNLK	300	
QY	301	KLEODDTKRITISPLADELTYNBERPTIVKGNVETCKAKAAEELMKKIRSEYENDIASML	360	
Db	301	KLEODDTKRITISPLADELTYNBERPTIVKGNVETCKAKAAEELMKKIRSEYENDIASML	360	
QY	361	QAHLLPGNLNALGEPPTSGMPPTSGSPSAMPVYPOEEOSETYVHOFTPLSVGAT	420	



Db 361 QAHILPGLNALGLFPPTSGMPPTSGPSAMTPPYQFQSETEYVHOIFALSVGAI 420  
Qy 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPPEAQFKAQGRITYGKIEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPPEAQFKAQGRITYGKIEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGARVIGKGGKTVNELONLSAEVVPVPRQTDENDQVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGARVIGKGGKTVNELONLSAEVVPVPRQTDENDQVVKIT 540  
Qy 541 GHFYACQVAORKIOELITVOKHOQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORKIOELITVOKHOQOKALQSGPPQSRK 579

RESULT 8  
US-09-606-421B-176  
; Sequence 176, Application US/09606421B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skelky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606,421B  
; CURRENT FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-606-421B-176

Query Match 100.0%; Score 579; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Qy 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDSLVOYGVESCEQVNTDSEFA 120  
Db 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDSLVOYGVESCEQVNTDSEFA 120  
Qy 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGRLGGRSS 180  
Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGRLGGRSS 180  
Qy 181 ROGSPGVSOKPCDPLRLVPTQFVGAIIKGEKATIRNITKOTQSKIDVHREKNAAGAA 240  
Db 181 ROGSPGVSOKPCDPLRLVPTQFVGAIIKGEKATIRNITKOTQSKIDVHREKNAAGAA 240  
Qy 241 EKSTITLSTPEGTSACKSILEIMHKEADIKFTEIEPLKILAHNNFVGRILGEGRNILK 300  
Db 241 EKSTITLSTPEGTSACKSILEIMHKEADIKFTEIEPLKILAHNNFVGRILGEGRNILK 300  
Qy 301 KIEODTDTKITISPLQELITVNPBRTITVKGNETCAKAEELIMKKIRESEYNDIASMNL 360  
Db 301 KIEODTDTKITISPLQELITVNPBRTITVKGNETCAKAEELIMKKIRESEYNDIASMNL 360  
Qy 361 QAHILPGLNALGLFPPTSGMPPTSGPSAMTPPYQFQSETEYVHOIFALSVGAI 420  
Db 361 QAHILPGLNALGLFPPTSGMPPTSGPSAMTPPYQFQSETEYVHOIFALSVGAI 420

Qy 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPPEAQFKAQGRITYGKIEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPPEAQFKAQGRITYGKIEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGARVIGKGGKTVNELONLSAEVVPVPRQTDENDQVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGARVIGKGGKTVNELONLSAEVVPVPRQTDENDQVVKIT 540  
Qy 541 GHFYACQVAORKIOELITVOKHOQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORKIOELITVOKHOQOKALQSGPPQSRK 579

RESULT 9  
US-09-630-940A-176  
; Sequence 176, Application US/09630940A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skelky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455G10  
; CURRENT APPLICATION NUMBER: US/09/630,940A  
; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-630-940A-176

Query Match 100.0%; Score 579; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Qy 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDSLVOYGVESCEQVNTDSEFA 120  
Db 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDSLVOYGVESCEQVNTDSEFA 120  
Qy 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGRLGGRSS 180  
Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGRLGGRSS 180  
Qy 181 ROGSPGVSOKPCDPLRLVPTQFVGAIIKGEKATIRNITKOTQSKIDVHREKNAAGAA 240  
Db 181 ROGSPGVSOKPCDPLRLVPTQFVGAIIKGEKATIRNITKOTQSKIDVHREKNAAGAA 240  
Qy 241 EKSTITLSTPEGTSACKSILEIMHKEADIKFTEIEPLKILAHNNFVGRILGEGRNILK 300  
Db 241 EKSTITLSTPEGTSACKSILEIMHKEADIKFTEIEPLKILAHNNFVGRILGEGRNILK 300  
Qy 301 KIEODTDTKITISPLQELITVNPBRTITVKGNETCAKAEELIMKKIRESEYNDIASMNL 360  
Db 301 KIEODTDTKITISPLQELITVNPBRTITVKGNETCAKAEELIMKKIRESEYNDIASMNL 360  
Qy 361 QAHILPGLNALGLFPPTSGMPPTSGPSAMTPPYQFQSETEYVHOIFALSVGAI 420  
Db 361 QAHILPGLNALGLFPPTSGMPPTSGPSAMTPPYQFQSETEYVHOIFALSVGAI 420

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us-09-897-778-176.Oligo.rapm

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OY	421	IGKGGHITKLSFPAASAKITAPADAPAKRVYITITGPEAOFAKGGITKIKENPV	480
	421	IGKGGHITKLSFPAASAKITAPADAPAKRVYITITGPEAOFAKGGITKIKENPV	480
Db	421	IGKGGHITKLSFPAASAKITAPADAPAKRVYITITGPEAOFAKGGITKIKENPV	480
OY	481	SPKEEVKLEAHITVSPFAAGRTIGKGGATNELONLSAEVVPDPDITPENDOVYVKIT	540
	481	SPKEEVKLEAHITVSPFAAGRTIGKGGATNELONLSAEVVPDPDITPENDOVYVKIT	540
Db	481	SPKEEVKLEAHITVSPFAAGRTIGKGGATNELONLSAEVVPDPDITPENDOVYVKIT	540
OY	541	GHEFYACVAKRKITDELITLVYQHQOQAALDSGPPQSRK	579
	541	GHEFYACVAKRKITDELITLVYQHQOQAALDSGPPQSRK	579
Db	541	GHEFYACVAKRKITDELITLVYQHQOQAALDSGPPQSRK	579

```

RESULT 10
US-09-630-940B-176
; Sequence 176, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fager, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 20121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-630-940B-176

```

Query Match	Local Similarity	100.0%	Score 579	DB 20	Length 579
Best Local Similarity	100.0%	Pred. No. 0			
Matches 579	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	MNLYGNGNSEMAAPSDLESFFDOKATIPYSGFFLKTGYAFVCCDPDESNAIKATEALSGK	60		
Db	1	MNLYGNGNSEMAAPSDLESFFDOKATIPYSGFFLKTGYAFVCCDPDESNAIKATEALSGK	60		
QY	61	IELHGKPIEVEHSYKRRQIRKIQIRNIPPHLOWEVLDSLLVQYGVESCEQVNDSETA	120		
Db	61	IELHGKPIEVEHSYKRRQIRKIQIRNIPPHLOWEVLDSLLVQYGVESCEQVNDSETA	120		
QY	121	VWVWYSSSKDQARALDKLNGFLENFTLKVAYIPDEMAQONPQLQPPGRGGLGQSSS	180		
Db	121	VWVWYSSSKDQARALDKLNGFLENFTLKVAYIPDEMAQONPQLQPPGRGGLGQSSS	180		
QY	181	ROGSPESYKSKPCDDPLRLVLPQYGVGAILGKGAIRNITQYOSKIDVHKREMGAA	240		
Db	181	ROGSPESYKSKPCDDPLRLVLPQYGVGAILGKGAIRNITQYOSKIDVHKREMGAA	240		
QY	241	EXSTITLSTPGTSAACKSTLEITMKREADIKFTEELPLKILAHNNFVGRILGKEGRNLK	300		
Db	241	EXSTITLSTPGTSAACKSTLEITMKREADIKFTEELPLKILAHNNFVGRILGKEGRNLK	300		
QY	301	KIEODTDKRTIISPLQELTYLNERTIVKGNVYTCCKAAKEELMKIKRESEENDIASMNL	360		
Db	301	KIEODTDKRTIISPLQELTYLNERTIVKGNVYTCCKAAKEELMKIKRESEENDIASMNL	360		
QY	361	QAHILPGLNALGALPPTSGMPPTSCSPBAMPPYPOFDESETEYWHOTIPALSYGAI	420		
Db	361	QAHILPGLNALGALPPTSGMPPTSCSPBAMPPYPOFDESETEYWHOTIPALSYGAI	420		

QY	421	IGKGGHIIKOLSFSAASAKIKIPAPAPAKRMVITITGPEEAFKNOGRTGKIKENFV	480
QY	421	IGKGGHIIKOLSFSAASAKIKIPAPAPAKRMVITITGPEEAFKNOGRTGKIKENFV	480
Db	421	IGKGGHIIKOLSFSAASAKIKIPAPAPAKRMVITITGPEEAFKNOGRTGKIKENFV	480
QY	481	SPKEEVLLEHIVPSEFAGRIGKGTNELONLSAEVVPDPDPDNDVVYK	540
Db	481	SPKEEVLLEHIVPSEFAGRIGKGTNELONLSAEVVPDPDPDNDVVYK	540
QY	541	GHEFACQVAKRKTOELITQVQHQQAKLDSGPPSRK	579
Db	541	GHEFACQVAKRKTOELITQVQHQQAKLDSGPPSRK	579

```

RESULT 11
US-09-662-786-176
? Sequence 176, Application US/09662786
? GENERAL INFORMATION:
? APPLICANT: Wang, Tongtong
? APPLICANT: Pan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Ajun
? APPLICANT: Skeiky, Yasir A. W.
? APPLICANT: Henderson Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.455C12
? CURRENT APPLICATION NUMBER: US/09/662,786
? CURRENT FILING DATE: 2000-09-15
? NUMBER OF SEQ ID NOS: 381
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 176
? LENGTH: 579
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-662-786-176

```

	Query Match	100.0%	Score 579	DB	Length 579
	Best Local Similarity	100.0%	Prod. NO. 0		
	Matches 579	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MKKLTIGLSNNAAPSDLESIFRKDAKIPVSGPFLVKTGAIVDCDESMALKATIALSGK	60		
DB	1	MKKLTIGLSNNAAPSDLESIFRKDAKIPVSGPFLVKTGAIVDCDESMALKATIALSGK	60		
QY	61	IELHGKPIEVEHVSYPKKRORIRKIQIRNIPPHIQEIVDLSILVQGVGESCEQVNTDETA	120		
DB	61	IELHGKPIEVEHVSYPKKRORIRKIQIRNIPPHIQEIVDLSILVQGVGESCEQVNTDETA	120		
QY	121	VVNVTYSSKQDARQALDKLNGFOLSNFTLKVAIYIPDEMAAQNPILOQRRGRIGQGCCS	180		
DB	121	VVNVTYSSKQDARQALDKLNGFOLSNFTLKVAIYIPDEMAAQNPILOQRRGRIGQGCCS	180		
QY	181	RGSGSGYSKQKRDPIRLYLVPQFVAILIGKSGATIRNITKQTSKIDYHKKENGA	240		
DB	181	RGSGSGYSKQKRDPIRLYLVPQFVAILIGKSGATIRNITKQTSKIDYHKKENGA	240		
QY	241	EKSITILSPDEGTSAAKCSILEIMHKEADIKFEEIPIKLIAHNNFVGRILGKEGRNKK	300		
DB	241	EKSITILSPDEGTSAAKCSILEIMHKEADIKFEEIPIKLIAHNNFVGRILGKEGRNKK	300		
QY	301	KIEQDPTKTTIPIELVELYPERKTIYKQNVETAKKAEEIIMKKIKESYEENDIASMNL	360		
DB	301	KIEQDPTKTTIPIELVELYPERKTIYKQNVETAKKAEEIIMKKIKESYEENDIASMNL	360		
QY	361	QAHILPGINATNAGLPPPTSGMPPTSGPSAMTPREYPOEEOSETFYHQCITALSAGAI	420		
DB	361	QAHILPGINATNAGLPPPTSGMPPTSGPSAMTPREYPOEEOSETFYHQCITALSAGAI	420		

QY 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVVMVITITGPEAOFKAGRIYGIKEENVV 480  
| | | | |  
Db 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVVMVITITGPEAOFKAGRIYGIKEENVV 480  
QY 481 SPKEEVKLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPRDÖTPDENDÖVVKIT 540  
| | | | |  
Db 481 SPKEEVKLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPRDÖTPDENDÖVVKIT 540  
QY 541 GHFYACQVAORRKIOEILITOVKHOQOKALOSGPPÖSRK 579  
| | | | |  
Db 541 GHFYACQVAORRKIOEILITOVKHOQOKALOSGPPÖSRK 579

## RESULT 12

us-09-685-696-176  
; Sequence 176, Application us/09685696  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Ligu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaltanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C13  
; CURRENT APPLICATION NUMBER: us/09/685.696  
; CURRENT FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FASTSEQ for windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
us-09-685-696-176

Query Match 100.0%; Score 579; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
| | | | |  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
QY 61 IELHGKPIEVEHSVPKRRIRIKLOIRNIPHLÖMEVLDLÖVGYVESCEÖYNTDSE7A 120  
| | | | |  
Db 61 IELHGKPIEVEHSVPKRRIRIKLOIRNIPHLÖMEVLDLÖVGYVESCEÖYNTDSE7A 120  
QY 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
| | | | |  
Db 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
QY 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
| | | | |  
Db 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
QY 181 ROGSPGVSÖKÖPCDLPRLLVPTÖFVGAIIÖKEGATIRNITÖKÖSDIVHÖKENAGAA 240  
| | | | |  
Db 181 ROGSPGVSÖKÖPCDLPRLLVPTÖFVGAIIÖKEGATIRNITÖKÖSDIVHÖKENAGAA 240  
QY 241 EKSTITLSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEILPÖKILAHNNVÖGRLÖKEGRNLK 300  
| | | | |  
Db 241 EKSTITLSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEILPÖKILAHNNVÖGRLÖKEGRNLK 300  
QY 301 KÖEÖDÖTKRITISPLÖEILTYNÖPERTIVKÖNVETÖKAKAEÖEIMKKIRÖSEYENDIASMNL 360  
| | | | |  
Db 301 KÖEÖDÖTKRITISPLÖEILTYNÖPERTIVKÖNVETÖKAKAEÖEIMKKIRÖSEYENDIASMNL 360  
QY 361 ÖAHLIPÖGLNLAÖGLFÖPTSGMÖPPTSGÖPSAMÖPPYÖPÖFÖSÖETÖVHÖFIPALSVGAI 420  
| | | | |  
Db 361 ÖAHLIPÖGLNLAÖGLFÖPTSGMÖPPTSGÖPSAMÖPPYÖPÖFÖSÖETÖVHÖFIPALSVGAI 420

QY 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVVMVITITGPEAOFKAGRIYGIKEENVV 480  
| | | | |  
Db 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVVMVITITGPEAOFKAGRIYGIKEENVV 480  
QY 481 SPKEEVKLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPRDÖTPDENDÖVVKIT 540  
| | | | |  
Db 481 SPKEEVKLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPRDÖTPDENDÖVVKIT 540  
QY 541 GHFYACQVAORRKIOEILITOVKHOQOKALOSGPPÖSRK 579  
| | | | |  
Db 541 GHFYACQVAORRKIOEILITOVKHOQOKALOSGPPÖSRK 579

## RESULT 13

us-09-735-705-176  
; Sequence 176, Application us/09735705  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Ligu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaltanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: us/09/735.705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FASTSEQ for windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
us-09-735-705-176

Query Match 100.0%; Score 579; DB 21; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
| | | | |  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
QY 61 IELHGKPIEVEHSVPKRRIRIKLOIRNIPHLÖMEVLDLÖVGYVESCEÖYNTDSE7A 120  
| | | | |  
Db 61 IELHGKPIEVEHSVPKRRIRIKLOIRNIPHLÖMEVLDLÖVGYVESCEÖYNTDSE7A 120  
QY 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
| | | | |  
Db 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
QY 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
| | | | |  
Db 121 VVNVTYSSKDOARÖALDKLNGFÖLENTLKVAYIPDEMAQÖNPLÖQPRGRRLGÖRGSS 180  
QY 181 ROGSPGVSÖKÖPCDLPRLLVPTÖFVGAIIÖKEGATIRNITÖKÖSDIVHÖKENAGAA 240  
| | | | |  
Db 181 ROGSPGVSÖKÖPCDLPRLLVPTÖFVGAIIÖKEGATIRNITÖKÖSDIVHÖKENAGAA 240  
QY 241 EKSTITLSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEILPÖKILAHNNVÖGRLÖKEGRNLK 300  
| | | | |  
Db 241 EKSTITLSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEILPÖKILAHNNVÖGRLÖKEGRNLK 300  
QY 301 KÖEÖDÖTKRITISPLÖEILTYNÖPERTIVKÖNVETÖKAKAEÖEIMKKIRÖSEYENDIASMNL 360  
| | | | |  
Db 301 KÖEÖDÖTKRITISPLÖEILTYNÖPERTIVKÖNVETÖKAKAEÖEIMKKIRÖSEYENDIASMNL 360  
QY 361 ÖAHLIPÖGLNLAÖGLFÖPTSGMÖPPTSGÖPSAMÖPPYÖPÖFÖSÖETÖVHÖFIPALSVGAI 420  
| | | | |  
Db 361 ÖAHLIPÖGLNLAÖGLFÖPTSGMÖPPTSGÖPSAMÖPPYÖPÖFÖSÖETÖVHÖFIPALSVGAI 420

Qy	421	IKQGOHITKOLSEFPAASIKIPADPAKVRVITITGPEKQKAGRIYKITEENFV	480
Qy	421	IKQGOHITKOLSEFPAASIKIPADPAKVRVITITGPEKQKAGRIYKITEENFV	480
Db	421	IKQGOHITKOLSEFPAASIKIPADPAKVRVITITGPEKQKAGRIYKITEENFV	480
Qy	481	SPKEEVKLEAHIVPSPFAAGRVITGKGTNELONLSANEVVRPDOTPENDOVYVIT	540
Db	481	SPKEEVKLEAHIVPSPFAAGRVITGKGTNELONLSANEVVRPDOTPENDOVYVIT	540
Qy	541	GHEFYACQYAAQRKIQELITVYKOHQOAKALDSGPPSSRRK	579
Db	541	GHEFYACQYAAQRKIQELITVYKOHQOAKALDSGPPSSRRK	579

```

RESULT 14
US-09-791-537-49019
: Sequence 49019, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Bionomix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 49019
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-791-537-49019

```

```
OY      541 GHTYACQVAQRKIDIELTVYKHQQDALKSGPPOSRRK .579
        |||||
Db       541 GHTYACQVAQRKIDIELTVYKHQQDALKSGPPOSRRK 579
```

```

RESULT 15
US-09-850-716-176
Sequence 176, Application us/09850716
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil W.
APPLICANT: Reller, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C13
CURRENT APPLICATION NUMBER: US/09/850,716
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716-176

```

Db 481 SPKEEVKLEAHIRVPSPFAGRVIGKSGKTVNELQNLSAEVVVPRDPTPENDQVVVKIT 540

OY 541 GHFYACQVAQRKIOEILITQYKHQOQKALQSGPPQSRK 579

Db 541 GHFYACQVAQRKIOEILITQYKHQOQKALQSGPPQSRK 579

Search completed: April 16, 2003, 16:45:11  
Job time : 395.655 secs





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Qy 361 QAHILIGLNLNLGLFPTSGMPPTSGPPSAMTPPYQFQSETEVTHOFTIPALSVGAI 420
Db 361 QAHILIGLNLNLGLFPTSGMPPTSGPPSAMTPPYQFQSETEVTHOFTIPALSVGAI 420
Qy 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQNLSSAEVYVPRDTPENDQVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQNLSSAEVYVPRDTPENDQVYVKIT 540
Qy 541 GHFYACQVAKRKIDIELTVYKQHOQKALQSGPQSRKK 579
Db 541 GHFYACQVAKRKIDIELTVYKQHOQKALQSGPQSRKK 579

RESULT 2
US-10-348-119-255
; Sequence 255, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348,119
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 255
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-119-255

Query Match 100.0%; Score 579; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMLKAIEALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMLKAIEALSCK 60
Qy 61 IELHGKPIEVESHVYKRRIRKIQIRNIPPHQWELDSLVOYGVSECEQVNTDSETA 120
Db 61 IELHGKPIEVESHVYKRRIRKIQIRNIPPHQWELDSLVOYGVSECEQVNTDSETA 120
Qy 121 VVAVTVSSKQARQALDLKNGFOLNFTLKVAIIPDEMAAQONPDAQPRGRGLGRCSS 180
Db 121 VVAVTVSSKQARQALDLKNGFOLNFTLKVAIIPDEMAAQONPDAQPRGRGLGRCSS 180
Qy 181 RQSPGSVSKQKPCDPLRLVLVPOFGAIIKEGATIRNTTKOTQSKIDVHKKENAGAA 240
Db 181 RQSPGSVSKQKPCDPLRLVLVPOFGAIIKEGATIRNTTKOTQSKIDVHKKENAGAA 240
Qy 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEIEIPKLILAHNNFVGLIKEGRNK 300
Db 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEIEIPKLILAHNNFVGLIKEGRNK 300
Qy 301 KIEQDPTDKITITSPLOELTYNPERTTYKGVNVCARAEIEIKKIRRESYENDIASNML 360
Db 301 KIEQDPTDKITITSPLOELTYNPERTTYKGVNVCARAEIEIKKIRRESYENDIASNML 360
Qy 361 QAHILIGLNLNLGLFPTSGMPPTSGPPSAMTPPYQFQSETEVTHOFTIPALSVGAI 420
Db 361 QAHILIGLNLNLGLFPTSGMPPTSGPPSAMTPPYQFQSETEVTHOFTIPALSVGAI 420
Qy 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
```

```
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQNLSSAEVYVPRDTPENDQVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQNLSSAEVYVPRDTPENDQVYVKIT 540
Qy 541 GHFYACQVAKRKIDIELTVYKQHOQKALQSGPQSRKK 579
Db 541 GHFYACQVAKRKIDIELTVYKQHOQKALQSGPQSRKK 579

RESULT 3
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match 95.5%; Score 553; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMLKAIEALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMLKAIEALSCK 60
Qy 61 IELHGKPIEVESHVYKRRIRKIQIRNIPPHQWELDSLVOYGVSECEQVNTDSETA 120
Db 61 IELHGKPIEVESHVYKRRIRKIQIRNIPPHQWELDSLVOYGVSECEQVNTDSETA 120
Qy 121 VVAVTVSSKQARQALDLKNGFOLNFTLKVAIIPDEMAAQONPDAQPRGRGLGRCSS 180
Db 121 VVAVTVSSKQARQALDLKNGFOLNFTLKVAIIPDEMAAQONPDAQPRGRGLGRCSS 180
Qy 181 RQSPGSVSKQKPCDPLRLVLVPOFGAIIKEGATIRNTTKOTQSKIDVHKKENAGAA 240
Db 181 RQSPGSVSKQKPCDPLRLVLVPOFGAIIKEGATIRNTTKOTQSKIDVHKKENAGAA 240
Qy 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEIEIPKLILAHNNFVGLIKEGRNK 300
Db 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEIEIPKLILAHNNFVGLIKEGRNK 300
Qy 301 KIEQDPTDKITITSPLOELTYNPERTTYKGVNVCARAEIEIKKIRRESYENDIASNML 360
Db 301 KIEQDPTDKITITSPLOELTYNPERTTYKGVNVCARAEIEIKKIRRESYENDIASNML 360
Qy 361 QAHILIGLNLNLGLFPTSGMPPTSGPPSAMTPPYQFQSETEVTHOFTIPALSVGAI 420
Db 361 QAHILIGLNLNLGLFPTSGMPPTSGPPSAMTPPYQFQSETEVTHOFTIPALSVGAI 420
Qy 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVYITGPPEAQKAGRIYGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQNLSSAEVYVPRDTPENDQVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQNLSSAEVYVPRDTPENDQVYVKIT 540
Qy 541 GHFYACQVAKRKI 553
Db 541 GHFYACQVAKRKI 553
```



```
RESULT 4
US-09-724-676A-92918
; Sequence 92918, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92918
```

```
Query Match          95.5%; Score 553; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGAFVDCPDDESMALKATEALS 60
   |||||||
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGAFVDCPDDESMALKATEALS 60
QY 61 IELHGKPIEVEHSPVKRQRIKLOIRNIPHLQMEVLDLSLVGYGVSECEQVNTDSE 120
   |||||||
DB 61 IELHGKPIEVEHSPVKRQRIKLOIRNIPHLQMEVLDLSLVGYGVSECEQVNTDSE 120
QY 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
   |||||||
DB 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
QY 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
   |||||||
DB 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
QY 181 RQSGSGSVSKQKPCDPLRLVPTQFVGALIGEGATIRNITQOTSKIDVHRKENAGA 240
   |||||||
DB 181 RQSGSGSVSKQKPCDPLRLVPTQFVGALIGEGATIRNITQOTSKIDVHRKENAGA 240
QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGRILKEGR 300
   |||||||
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGRILKEGR 300
QY 301 KIEODTDTKITISPLQELTLYNPERTITVKGNETCAKAEEMKIRI 360
   |||||||
DB 301 KIEODTDTKITISPLQELTLYNPERTITVKGNETCAKAEEMKIRI 360
QY 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETVHOFTALSV 420
   |||||||
DB 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETVHOFTALSV 420
QY 421 IKGQGHIKQLSRFAGASIKIAPAEAPDAKVRMYITGPPEAQFKAQRIYK 480
   |||||||
DB 421 IKGQGHIKQLSRFAGASIKIAPAEAPDAKVRMYITGPPEAQFKAQRIYK 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQMLSSAEVVPDPDQTPDEND 540
   |||||||
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQMLSSAEVVPDPDQTPDEND 540
QY 541 GHFYACQVAQRKI 553
   |||||||
DB 541 GHFYACQVAQRKI 553
```

```
RESULT 5
US-09-724-676-92916
; Sequence 92916, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92916
```

```
Query Match          80.7%; Score 467; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGAFVDCPDDESMALKATEALS 60
   |||||||
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGAFVDCPDDESMALKATEALS 60
QY 61 IELHGKPIEVEHSPVKRQRIKLOIRNIPHLQMEVLDLSLVGYGVSECEQVNTDSE 120
   |||||||
DB 61 IELHGKPIEVEHSPVKRQRIKLOIRNIPHLQMEVLDLSLVGYGVSECEQVNTDSE 120
QY 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
   |||||||
DB 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
QY 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
   |||||||
DB 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
QY 181 RQSGSGSVSKQKPCDPLRLVPTQFVGALIGEGATIRNITQOTSKIDVHRKENAGA 240
   |||||||
DB 181 RQSGSGSVSKQKPCDPLRLVPTQFVGALIGEGATIRNITQOTSKIDVHRKENAGA 240
QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGRILKEGR 300
   |||||||
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGRILKEGR 300
QY 301 KIEODTDTKITISPLQELTLYNPERTITVKGNETCAKAEEMKIRI 360
   |||||||
DB 301 KIEODTDTKITISPLQELTLYNPERTITVKGNETCAKAEEMKIRI 360
QY 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETVHOFTALSV 420
   |||||||
DB 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETVHOFTALSV 420
QY 421 IKGQGHIKQLSRFAGASIKIAPAEAPDAKVRMYITGPPEAQFKAQRIYK 480
   |||||||
DB 421 IKGQGHIKQLSRFAGASIKIAPAEAPDAKVRMYITGPPEAQFKAQRIYK 480
```

```
RESULT 6
US-09-724-676A-92916
; Sequence 92916, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92916
```

```
Query Match          80.7%; Score 467; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGAFVDCPDDESMALKATEALS 60
   |||||||
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGAFVDCPDDESMALKATEALS 60
QY 61 IELHGKPIEVEHSPVKRQRIKLOIRNIPHLQMEVLDLSLVGYGVSECEQVNTDSE 120
   |||||||
DB 61 IELHGKPIEVEHSPVKRQRIKLOIRNIPHLQMEVLDLSLVGYGVSECEQVNTDSE 120
QY 121 VVNVTVSSKDQARQALDKLNGFQLENTFLKVAYIPDEMAAQNPLQOPRGRRGLG 180
   |||||||
```

```
|||||
Db 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPQPRGRGLGGRSS 180
QY 181 RQSGPSGYSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKQTSKIDVHKENAGAA 240
|||
Db 181 RQSGPSGYSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKQTSKIDVHKENAGAA 240
QY 241 EKSTIIITSTPGTSACKSILETMHKEADIKFTEIPLKTLANNFVGLIGKEGRNLK 300
|||
Db 241 EKSTIIITSTPGTSACKSILETMHKEADIKFTEIPLKTLANNFVGLIGKEGRNLK 300
QY 301 KIEODPTKITISPLQELLYNPERTIVKGNVETCAKAEIEIKK1RESYENDIASMNL 360
|||
Db 301 KIEODPTKITISPLQELLYNPERTIVKGNVETCAKAEIEIKK1RESYENDIASMNL 360
QY 361 QAHILPGLNLTALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
|||
Db 361 QAHILPGLNLTALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
QY 421 IKGQGHITKQLSRFAGASIKIAPAEAPDAKVMVITTPGPAQFKAQ 467
|||
Db 421 IKGQGHITKQLSRFAGASIKIAPAEAPDAKVMVITTPGPAQFKAQ 467

RESULT 7
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 579
; TYPE: PRN
; ORGANISM: primate
US-10-313-986-484

Query Match 68.7%; Score 398; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 NAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGKIELHGRITVE 71
Db 12 NAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGKIELHGRITVE 71
QY 72 HSVKROIRIKLQIRNIPHLQWEVLDLVOYGVESCEQVNTDSEAVVNTYSSKQ 131
Db 72 HSVKROIRIKLQIRNIPHLQWEVLDLVOYGVESCEQVNTDSEAVVNTYSSKQ 131
QY 132 AROALDKLNGFQLENFTLKVAIIPDEMAAQNLPQPRGRGLGGRSSRQSGPSGYSKQ 191
Db 132 AROALDKLNGFQLENFTLKVAIIPDEMAAQNLPQPRGRGLGGRSSRQSGPSGYSKQ 191
QY 192 KPCDPLRLVPTQFVGAIIGKEGATIRNTKQTSKIDVHKENAGAAEKSTIIITSTPE 251
Db 192 KPCDPLRLVPTQFVGAIIGKEGATIRNTKQTSKIDVHKENAGAAEKSTIIITSTPE 251
QY 252 GTSACKSILEIMHKEADIKFTEIPLKTLANNFVGLIGKEGRNLKIEODPTKIT 311
Db 252 GTSACKSILEIMHKEADIKFTEIPLKTLANNFVGLIGKEGRNLKIEODPTKIT 311
QY 312 ISPLQELLYNPERTIVKGNVETCAKAEIEIKK1RESYENDIASMNLQAHILPGLNLT 371
Db 312 ISPLQELLYNPERTIVKGNVETCAKAEIEIKK1RESYENDIASMNLQAHILPGLNLT 371
```

```
QY 372 ALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVH 409
Db 372 ALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVH 409

RESULT 8
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-313-986-348

Query Match 65.1%; Score 377; DB 6; Length 579;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGK 60
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGK 60
QY 61 IELHGRPLEVHSHVPRKQIRIKLQIRNIPHLQWEVLDLVOYGVESCEQVNTDSEAV 120
Db 61 IELHGRPLEVHSHVPRKQIRIKLQIRNIPHLQWEVLDLVOYGVESCEQVNTDSEAV 120
QY 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPQPRGRGLGGRSS 180
Db 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPQPRGRGLGGRSS 180
QY 181 RQSGPSGYSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKQTSKIDVHKENAGAA 240
Db 181 RQSGPSGYSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKQTSKIDVHKENAGAA 240
QY 241 EKSTIIITSTPGTSACKSILETMHKEADIKFTEIPLKTLANNFVGLIGKEGRNLK 300
Db 241 EKSTIIITSTPGTSACKSILETMHKEADIKFTEIPLKTLANNFVGLIGKEGRNLK 300
QY 301 KIEODPTKITISPLQELLYNPERTIVKGNVETCAKAEIEIKK1RESYENDIASMNL 360
Db 301 KIEODPTKITISPLQELLYNPERTIVKGNVETCAKAEIEIKK1RESYENDIASMNL 360
QY 361 QAHILPGLNLTALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
Db 361 QAHILPGLNLTALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
QY 421 IKGQGHITKQLSRFAGASIKIAPAEAPDAKVMVITTPGPAQFKAQGRYIGKEENFV 480
Db 421 IKGQGHITKQLSRFAGASIKIAPAEAPDAKVMVITTPGPAQFKAQGRYIGKEENFV 480
QY 481 SPKEEVLEHINIVPFAAGRIYIGGKTVNELNLSAEVYVPRDTPENDQVYVKT 540
Db 481 SPKEEVLEHINIVPFAAGRIYIGGKTVNELNLSAEVYVPRDTPENDQVYVKT 540
QY 541 GHFACQVAORAKIOELITVOYKHOQKALQSGPPQSRK 579
Db 541 GHFACQVAORAKIOELITVOYKHOQKALQSGPPQSRK 579
```

## RESULT 9

US-10-313-986-446  
 ; Sequence 446, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C19  
 ; CURRENT APPLICATION NUMBER: US/10/313.986  
 ; CURRENT FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 560  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 446  
 ; LENGTH: 579  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-313-986-446

Query Match 65.1%; Score 377; DB 6; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFPDPPESWALKAIEALSGK 60  
 DB 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFPDPPESWALKAIEALSGK 60  
 QY 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELVDSLVOYGVESEQVNTDSETA 120  
 DB 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELVDSLVOYGVESEQVNTDSETA 120  
 QY 121 VVNVYSSKDOARQALDKLNGFOLENTLKVAYIPDEMAAQNPLQOPRCRGLGGRSS 180  
 DB 121 VVNVYSSKDOARQALDKLNGFOLENTLKVAYIPDEMAAQNPLQOPRCRGLGGRSS 180  
 QY 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 DB 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 QY 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGKGRNLK 300  
 DB 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGKGRNLK 300  
 QY 301 KIEQDTDKITISPLQELTLYNPERTITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
 DB 301 KIEQDTDKITISPLQELTLYNPERTITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
 QY 361 QAHILPGNLNALGLPPTSGMPPTSGPPSAMTPPYPOEJOSETETVHOFIPALSVGAI 420  
 DB 361 QAHILPGNLNALGLPPTSGMPPTSGPPSAMTPPYPOEJOSETETVHOFIPALSVGAI 420  
 QY 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 DB 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNEONLSSAEVVPVPRQTPDENQVYVVKIT 540  
 DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNEONLSSAEVVPVPRQTPDENQVYVVKIT 540  
 QY 541 GHFYACQVAQRKIOEILTVQKHQOQKALOSGPQSRK 579  
 DB 541 GHFYACQVAQRKIOEILTVQKHQOQKALOSGPQSRK 579

RESULT 10  
 US-10-313-986-449  
 ; Sequence 449, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C19  
 ; CURRENT APPLICATION NUMBER: US/10/313.986  
 ; CURRENT FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 560  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 449  
 ; LENGTH: 579  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-313-986-449

Query Match 65.1%; Score 377; DB 6; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFPDPPESWALKAIEALSGK 60  
 DB 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFPDPPESWALKAIEALSGK 60  
 QY 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELVDSLVOYGVESEQVNTDSETA 120  
 DB 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELVDSLVOYGVESEQVNTDSETA 120  
 QY 121 VVNVYSSKDOARQALDKLNGFOLENTLKVAYIPDEMAAQNPLQOPRCRGLGGRSS 180  
 DB 121 VVNVYSSKDOARQALDKLNGFOLENTLKVAYIPDEMAAQNPLQOPRCRGLGGRSS 180  
 QY 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 DB 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 QY 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGKGRNLK 300  
 DB 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGKGRNLK 300  
 QY 301 KIEQDTDKITISPLQELTLYNPERTITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
 DB 301 KIEQDTDKITISPLQELTLYNPERTITVKGNETCAKAEELIMKKIRESEYENDIASMNL 360  
 QY 361 QAHILPGNLNALGLPPTSGMPPTSGPPSAMTPPYPOEJOSETETVHOFIPALSVGAI 420  
 DB 361 QAHILPGNLNALGLPPTSGMPPTSGPPSAMTPPYPOEJOSETETVHOFIPALSVGAI 420  
 QY 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 DB 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNEONLSSAEVVPVPRQTPDENQVYVVKIT 540  
 DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNEONLSSAEVVPVPRQTPDENQVYVVKIT 540  
 QY 541 GHFYACQVAQRKIOEILTVQKHQOQKALOSGPQSRK 579  
 DB 541 GHFYACQVAQRKIOEILTVQKHQOQKALOSGPQSRK 579

RESULT 11  
 US-10-313-986-480  
 ; Sequence 480, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C19

;; CURRENT APPLICATION NUMBER: US/10/313.986  
;; CURRENT FILING DATE: 2002-12-04  
;; NUMBER OF SEQ ID NOS: 560  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 480  
;; LENGTH: 579  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-313-986-480

Query Match 65.1%; Score 377; DB 6; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNSNAAPSDLESTIFKDAKIPVSGPIVKTGYAVDCCPDSEMLKATEALSGK 60  
DB 1 MNKLYIGNSNAAPSDLESTIFKDAKIPVSGPIVKTGYAVDCCPDSEMLKATEALSGK 60  
QY 61 IELHCKPIEVEHSVPRKRIKQIRNIPHLQWEYLSLVQYGVVESCQVNTDSETA 120  
DB 61 IELHCKPIEVEHSVPRKRIKQIRNIPHLQWEYLSLVQYGVVESCQVNTDSETA 120  
QY 121 VNVVTYSSKQARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQDPGRGRGLGORGSS 180  
DB 121 VNVVTYSSKQARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQDPGRGRGLGORGSS 180  
QY 181 RQSGPSVSKOKPCDPLRLVPTQFVGALIGKEGATINIKOTQSKIDVHRKEMGAA 240  
DB 181 RQSGPSVSKOKPCDPLRLVPTQFVGALIGKEGATINIKOTQSKIDVHRKEMGAA 240  
QY 241 EKSTITLSPREGTSAACKSILEIMHKEADIKFTEEIPKLIHNNFVGRILGKEGNL 300  
DB 241 EKSTITLSPREGTSAACKSILEIMHKEADIKFTEEIPKLIHNNFVGRILGKEGNL 300  
QY 301 KIQODPTKITISPLQELTLNPERTTVKGNVETCAKAEEMMKIRESEYENDIASMNL 360  
DB 301 KIQODPTKITISPLQELTLNPERTTVKGNVETCAKAEEMMKIRESEYENDIASMNL 360  
QY 361 QAHILIGLNLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420  
DB 361 QAHILIGLNLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420  
QY 421 IGKOGHITKOLSRFGASIKIAPADAPAKRYVITIGPEAOFRKOGRIYKIKEENFV 480  
DB 421 IGKOGHITKOLSRFGASIKIAPADAPAKRYVITIGPEAOFRKOGRIYKIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVNEQLNLSAEVVPVPRDQTPDEMDVYVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVNEQLNLSAEVVPVPRDQTPDEMDVYVKIT 540  
QY 541 GHFYACQVAORRQIOELITQVKKHQQOKALQSGPPQSRK 579  
DB 541 GHFYACQVAORRQIOELITQVKKHQQOKALQSGPPQSRK 579

RESULT 12  
US-10-313-986-486  
;; Sequence 486, Application US/10313986  
;; GENERAL INFORMATION:  
;; APPLICANT: Foy, Teresa M.  
;; APPLICANT: McNabb, Andria  
;; APPLICANT: Watanabe, Yoshihiro  
;; APPLICANT: Reed, Steven G.  
;; APPLICANT: Wang, Tonglong  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.455C19  
;; CURRENT APPLICATION NUMBER: US/10/313.986  
;; CURRENT FILING DATE: 2002-12-04  
;; NUMBER OF SEQ ID NOS: 560  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 486  
;; LENGTH: 589

;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-313-986-486

Query Match 65.1%; Score 377; DB 6; Length 589;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNSNAAPSDLESTIFKDAKIPVSGPIVKTGYAVDCCPDSEMLKATEALSGK 60  
DB 1 MNKLYIGNSNAAPSDLESTIFKDAKIPVSGPIVKTGYAVDCCPDSEMLKATEALSGK 60  
QY 61 IELHCKPIEVEHSVPRKRIKQIRNIPHLQWEYLSLVQYGVVESCQVNTDSETA 120  
DB 61 IELHCKPIEVEHSVPRKRIKQIRNIPHLQWEYLSLVQYGVVESCQVNTDSETA 120  
QY 121 VNVVTYSSKQARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQDPGRGRGLGORGSS 180  
DB 121 VNVVTYSSKQARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQDPGRGRGLGORGSS 180  
QY 181 RQSGPSVSKOKPCDPLRLVPTQFVGALIGKEGATINIKOTQSKIDVHRKEMGAA 240  
DB 181 RQSGPSVSKOKPCDPLRLVPTQFVGALIGKEGATINIKOTQSKIDVHRKEMGAA 240  
QY 241 EKSTITLSPREGTSAACKSILEIMHKEADIKFTEEIPKLIHNNFVGRILGKEGNL 300  
DB 241 EKSTITLSPREGTSAACKSILEIMHKEADIKFTEEIPKLIHNNFVGRILGKEGNL 300  
QY 301 KIQODPTKITISPLQELTLNPERTTVKGNVETCAKAEEMMKIRESEYENDIASMNL 360  
DB 301 KIQODPTKITISPLQELTLNPERTTVKGNVETCAKAEEMMKIRESEYENDIASMNL 360  
QY 361 QAHILIGLNLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420  
DB 361 QAHILIGLNLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420  
QY 421 IGKOGHITKOLSRFGASIKIAPADAPAKRYVITIGPEAOFRKOGRIYKIKEENFV 480  
DB 421 IGKOGHITKOLSRFGASIKIAPADAPAKRYVITIGPEAOFRKOGRIYKIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVNEQLNLSAEVVPVPRDQTPDEMDVYVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRYIGKGTVNEQLNLSAEVVPVPRDQTPDEMDVYVKIT 540  
QY 541 GHFYACQVAORRQIOELITQVKKHQQOKALQSGPPQSRK 579  
DB 541 GHFYACQVAORRQIOELITQVKKHQQOKALQSGPPQSRK 579

RESULT 13  
US-10-313-986-427  
;; Sequence 427, Application US/10313986  
;; GENERAL INFORMATION:  
;; APPLICANT: Foy, Teresa M.  
;; APPLICANT: McNabb, Andria  
;; APPLICANT: Watanabe, Yoshihiro  
;; APPLICANT: Reed, Steven G.  
;; APPLICANT: Wang, Tonglong  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.455C19  
;; CURRENT APPLICATION NUMBER: US/10/313.986  
;; CURRENT FILING DATE: 2002-12-04  
;; NUMBER OF SEQ ID NOS: 560  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 427  
;; LENGTH: 586  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-313-986-427

Query Match 64.9%; Score 376; DB 6; Length 586;  
Best Local Similarity 99.7%; Pred. No. 0;

Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 2 NKLTYIGNSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSSMLKAIKALSGK 61
    |||||||
DB 9 NKLTYIGNSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSSMLKAIKALSGK 68
    |||||||
OY 62 ELHGKPIEVEHSVPKRQRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 121
    |||||||
DB 69 ELHGKPIEVEHSVPKRQRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 128
    |||||||
OY 122 VVNTYSSKDQARQALDKLNGOLENFTLKAYIIPDEMAAQNLOQPRGRGIGOGSSR 181
    |||||||
DB 129 VVNTYSSKDQARQALDKLNGOLENFTLKAYIIPDEMAAQNLOQPRGRGIGOGSSR 188
    |||||||
OY 182 QGSPGVSVKQKPCDLPRLPLVPTQFVGAIGKGGATIRNTKOTQSKIDVHRKENGAAE 241
    |||||||
DB 189 QGSPGVSVKQKPCDLPRLPLVPTQFVGAIGKGGATIRNTKOTQSKIDVHRKENGAAE 248
    |||||||
OY 242 KSTITLSTPECTSAACKSILEIMHKEADIKFTEELPLKILAHNNEFVGRIGKEGRNLK 301
    |||||||
DB 249 KSTITLSTPECTSAACKSILEIMHKEADIKFTEELPLKILAHNNEFVGRIGKEGRNLK 308
    |||||||
OY 302 IEODTDTKITISPLQELTIVNPERTIVKGNVETCAKAEIEIMKTIRESYENDIASMNIQ 361
    |||||||
DB 309 IEODTDTKITISPLQELTIVNPERTIVKGNVETCAKAEIEIMKTIRESYENDIASMNIQ 368
    |||||||
OY 362 AHLPLGLNLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFTPLASGATII 421
    |||||||
DB 369 AHLPLGLNLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFTPLASGATII 428
    |||||||
OY 422 GKOGCHIKQLSRFAGASIKIIPAEAPADAKVMVITTPPAOPKAGRIYKIKENEFVS 481
    |||||||
DB 429 GKOGCHIKQLSRFAGASIKIIPAEAPADAKVMVITTPPAOPKAGRIYKIKENEFVS 488
    |||||||
OY 482 PKEVKLEAHRVSPFAAGRTYKGGKTVNELNLSSAEVYVPRDQTPDENOVVYKRTG 541
    |||||||
DB 489 PKEVKLEAHRVSPFAAGRTYKGGKTVNELNLSSAEVYVPRDQTPDENOVVYKRTG 548
    |||||||
OY 542 HFYACOVAKRKTOELITOVKHOQOKALQSGPPQSRRK 579
    |||||||
DB 549 HFYACOVAKRKTOELITOVKHOQOKALQSGPPQSRRK 586
    |||||||

```

RESULT 14

US-09-724-676-92917  
; Sequence 92917, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; CURRENT APPLICATION NUMBER: 129181.4 Compugen

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92917

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676-92917

Query Match 23.1%; Score 134; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 8.4e-129;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSSMLKAIKALSGK 60
    |||||||
DB 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSSMLKAIKALSGK 60
    |||||||
OY 61 ELHGKPIEVEHSVPKRQRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
    |||||||
DB 61 ELHGKPIEVEHSVPKRQRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
    |||||||
OY 121 VVNTYSSKDQARQ 134

```

DB 121 VVNTYSSKDQARQ 134

RESULT 15

US-09-724-676A-92917

; Sequence 92917, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92917

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676A-92917

Query Match

Best Local Similarity 100.0%; Pred. No. 8.4e-129;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSSMLKAIKALSGK 60
    |||||||
DB 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSSMLKAIKALSGK 60
    |||||||
OY 61 ELHGKPIEVEHSVPKRQRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
    |||||||
DB 61 ELHGKPIEVEHSVPKRQRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
    |||||||
OY 121 VVNTYSSKDQARQ 134
    |||||||
DB 121 VVNTYSSKDQARQ 134
    |||||||

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Search completed: April 16, 2003, 16:47:24

Job time: 121.793 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:31:34 ; Search time 37.0788 Seconds  
(without alignments)  
1501.176 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579  
Sequence: 1 MNKLYIGNLSENAPSDLES.....VKHQOQKALQSGPPQSRK 579

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR-73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.4	242	2	G96994
2	8	1.4	311	2	A38558
3	8	1.4	324	2	AC0088
4	8	1.4	338	2	D95292
5	8	1.4	925	2	T02811
6	8	1.4	997	2	T43523
7	8	1.4	1000	2	S44898
8	8	1.4	1101	2	G70951
9	8	1.4	1198	2	B88279
10	8	1.4	1220	2	T19117
11	8	1.4	1472	2	B54774
12	8	1.4	1529	2	A59189
13	8	1.4	1704	2	S73163
14	8	1.4	1704	2	A59188
15	8	1.4	2201	2	A37774
16	8	1.4	3164	1	WMBE66
17	8	1.2	59	2	D84234
18	7	1.2	76	2	A11993
19	7	1.2	107	2	B72498
20	7	1.2	121	2	T47741
21	7	1.2	123	2	D71922
22	7	1.2	123	2	H64592
23	7	1.2	130	2	T50778
24	7	1.2	132	2	F97592
25	7	1.2	132	2	AB2814
26	7	1.2	139	1	B69486
27	7	1.2	146	1	R5BSLS
28	7	1.2	153	1	HHSY17
29	7	1.2	170	2	G75043

30	7	1.2	182	2	B35650	hypothetical 20k p
31	7	1.2	183	2	S56460	probable alpha hel
32	7	1.2	183	2	C91280	probable alpha hel
33	7	1.2	183	2	C68121	probable alpha hel
34	7	1.2	183	2	AD1056	conserved hypotnet
35	7	1.2	185	2	C71117	hypothetical prote
36	7	1.2	192	2	A72646	hypothetical prote
37	7	1.2	203	2	UC6113	meronocyte-specifi
38	7	1.2	232	2	G70738	probable FPE prote
39	7	1.2	239	1	D41316	flagellin B3 precu
40	7	1.2	239	2	G87265	conserved hypotnet
41	7	1.2	242	2	F87687	nucleotidyltransfe
42	7	1.2	279	2	T33429	hypothetical prote
43	7	1.2	285	2	T18689	hypothetical prote
44	7	1.2	286	2	F5104	hypothetical 31.3
45	7	1.2	286	2	C91132	hypothetical prote

#### ALIGNMENTS

RESULT 1  
G96994  
glycerol uptake facilitator protein, permease (imported) - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: G96994  
R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900, MUID:21359325, PMID:21359325  
A:Accession: G96994  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-242 <R>  
A:Cross-references: GB:AE001437; PDB:AAK78746.1; PID:g15023655; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0770  
C:Superfamily: glycerol facilitator protein

Query Match 1.4% Score 8; DB 2; Length 242;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 QFVGATIG 212  
DB 94 QFVGATIG 101

RESULT 2  
A38558  
interferon response element-binding factor 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 05-Nov-1999  
C:Accession: A38558  
R:Ryan, C.; Tamm, I  
Proc. Natl. Acad. Sci. U.S.A. 89, 144-148, 1991  
A:Title: Molecular cloning and characterization of interferon alpha/beta response e  
A:Reference number: A38558, MUID:91095416, PMID:1986360  
A:Accession: A38558  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-311 <Y>  
A:Cross-references: GB:A55290; NID:g194096; PID:AAA37884.1; PID:g194097  
C:Keywords: DNA binding; phosphoprotein; transcription regulation

Query Match 1.4% Score 8; DB 2; Length 311;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MNKLYIGNL 9

Db 106 NR11GNL 113

## RESULT 3

Probable flagellar motor switch protein [Imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 01-Mar-2002  
C:Accession: AC0088  
R:Parkhill, J.; Wren, B.W.; Thompson, N.R.; Tishball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AC0088  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-324 <RUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89566.1; PID:915978799; GSPDB:GN00175  
C:Genetics:  
A:Gene: fljG  
C:Superfamily: flagellar switch protein fljG

## Query Match

Best Local Similarity 100.0%; Pred. No. 10;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DQAROLD 137  
11111111  
Db 44 DQAROLD 51

## RESULT 4

Probable ABC transporter, permease Sma0467 [Imported] - Sinorhizobium meliloti (strain 1021)  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: D95292  
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, K.; Kaiman, M.J.; Keating, D.H.; Palm, G.; Peck, M.C.; Surzycski, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: D95292  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-938 <RUR>  
A:Cross-references: GB:AE006469; PIDN:AAK64902.1; PID:914523322; GSPDB:GN00165  
A:Experimental source: Strain 1021, megaplasmid pSymA, Abola, P.; Ampe, F.; Barloy-Hubler, F.; Gilbert, P.; Pinaud, A.; Long, S.R.; Hubler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chail, P.; Pinaud, A.; Davis, K.W.; Diano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.; Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebut, P.; Vandenbol, M.; Vorholter, J.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma0467  
A:Genome: plasmid

## Query Match

Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DSLVVOYG 105  
11111111  
Db 82 DSLVVOYG 89

## RESULT 5

DNA excision/repair protein, SNF2 and RAD26 DRP1 [Imported] - Leishmania major (str. 702811)  
C:Species: Leishmania major  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 19-May-2000  
R:Kryter, P.J.; Audlemann, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, R.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
A:Title: Leishmania major STR14110 chromosome has an unusual distribution of prote  
A:Accession: G81457  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-925 <PYL>  
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AA24634.1; PID:92995587; GSPDB  
A:Experimental source: strain MRCM/IL/81/Friedlin  
C:Genetics:  
A:Gene: DRP1  
A:Map position: 1

## Query Match

Best Local Similarity 100.0%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 PPTSCGP 390  
11111111  
Db 103 PPTSCGP 110

## RESULT 6

cut17 protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Jun-2000  
C:Accession: T43523; T41649; T41700  
R:Morishita, J.; Matsusaka, T.; Yanagida, M.  
A:Submitted to the EMBL data library, August 1999  
A:Description: Fission yeast cut17 is required for chromosome segregation.  
A:Reference number: Z22536  
A:Accession: T43523  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-997 <MOR>  
A:Cross-references: EMBL:AB031034; PIDN:BA483415.1  
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrett, B.G.  
A:Submitted to the EMBL data library, August 1998  
A:Reference number: Z22007  
A:Accession: T41649  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-997 <HAR>  
A:Cross-references: EMBL:AL031323; PIDN:CA420434.1; GSPDB:GN00068; SPDB:SPCC962.02c  
A:Experimental source: strain 972h, cosmid c902 Rajandream, M.A.; Barrett, B.G.  
A:Submitted to the EMBL data library, October 1999  
A:Accession: T41700  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 932-997 <MED>  
A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCC31B10.10c  
C:Genetics:  
A:Gene: cut17; SPCC962.02c; SPDB:SPCC31B10.10c  
A:Map position: 3L  
A:Intons: 43/3

## Query Match

Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 FTEIPPLK 280  
11111111  
Db 342 FTEIPPLK 349



## RESULT 7

S44898 ZK1236.3 protein - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001

C:Accession: S44898

R:Ravello, A.D.

submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the *C. elegans* cosmid ZK1236.

A:Reference number: S44622

A:Accession: S44898

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1000 &lt;EAV&gt;

A:Cross-references: EMBL:L13200; NID:g289748; PID:g289754

C:Genetics:

A:Introns: 56/3; 86/2; 189/3; 243/2; 669/3; 808/3; 984/3

## Query Match

Best Local Similarity 1.4%; Score 8; DB 2; Length 1000;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PSDLESTF 22

DB 568 PSDLESTF 575

## RESULT 8

G70951 probable ATP-dependent DNA helicase - *Mycobacterium tuberculosis* (strain H37RV)C:Species: *Mycobacterium tuberculosis*

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: G70951

R:COLE, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: G70951

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1101 &lt;COL&gt;

A:Cross-references: GB:AL021646; GB:AL123456; NID:g3242278; PID:CAA16666.1; PID:el24879

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV3201c

## Query Match

Best Local Similarity 1.4%; Score 8; DB 2; Length 1101;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ALGLFPPT 379

DB 18 ALGLFPPT 25

## RESULT 9

B88279 Protein C08H9.2 (imported) - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001

C:Accession: B88279

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see web sites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: B88279

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1198 &lt;STO&gt;

A:Cross-references: GB:chr\_II; PIDN:CAA91144.1; PID:g3874123; GSPDB:GN00020; CESP:C08

C:Genetics:

A:Gene: C08H9.2

A:Map position: 2

C:Superfamily: vlg11ln

## Query Match

Best Local Similarity 1.4%; Score 8; DB 2; Length 1198;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 GRIGKEG 296

DB 126 GRIGKEG 133

## RESULT 10

T19117 hypothetical protein C08H9.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T19117

R:Blöyd, C.

submitted to the EMBL Data Library, October 1995

A:Reference number: Z19074

A:Accession: T19117

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1220 &lt;WIL&gt;

A:Cross-references: EMBL:Z54342; PIDN:CAA91144.2; GSPDB:GN00020; CESP:C08H9.2

A:Experimental source: clone C08H9

C:Genetics:

A:Gene: CESP:C08H9.2

A:Map position: 2

A:Introns: 7/1; 560/3; 949/3; 1155/3

C:Superfamily: vlg11ln

## Query Match

Best Local Similarity 1.4%; Score 8; DB 2; Length 1220;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 GRIGKEG 296

DB 148 GRIGKEG 155

## RESULT 11

B54774 ATP binding cassette transporter ABC2 - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Feb-2001

C:Accession: B54774

R:Luciani, M.F.; Denicot, F.; Savary, S.; Mattei, M.G.; Chinini, G.

Genomics 21, 150-159, 1994

A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.

A:Reference number: A54774; MUID:94375008; PMID:8088782

A:Accession: B54774

A:Molecule type: mRNA

A:Residues: 1-1472 &lt;LUC&gt;

A:Cross-references: GB:X75927; NID:g495258; PIDN:CAA53531.1; PID:g495259

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

C:Keywords: ATP; nucleotide binding; P-loop

F:4-234/Domain: ATP-binding cassette homolog &lt;ABC1&gt;

F:61-68/Region: nucleotide-binding motif A (P-loop)

F:1108-1130/Domain: ATP-binding cassette homolog &lt;ABC2&gt;

F:1126-1133/Region: nucleotide-binding motif A (P-loop)

## Query Match

Best Local Similarity 1.4%; Score 8; DB 2; Length 1472;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 1111111111  
 Db 76 GLEPPTSG 83

## RESULT 12

A59189  
 ATP-binding cassette transporter - human (fragment)  
 N:Alternate names: KIAA1062 protein  
 C:Species: Homo sapiens (man)  
 C>Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 02-Jun-2000  
 C:Accession: A59189  
 R:Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirose, M.; Miyajima, N.; Tanaka, A.; Kotani, DNA Res. 6, 197-205, 1999  
 A:Title: Prediction of the coding sequences of unidentified human genes. XIV. The complete  
 A:Reference number: 223961; MUID:99397452; PMID:10470851  
 A:Accession: A59189  
 A>Status: preliminary: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1529 <KIX>  
 A:Cross-references: GB:AB028985; NID:q5689460; PIDN:BA03014.1; PID:d1046841; PID:q56894  
 A:Experimental source: chromosome 9; clone hJ03579; clone 11b p19nescriptII SK plus; t18  
 C:Genetics:  
 A:Map position: 9  
 A>Note: KIAA1062  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.4%; Score 8; DB 2; Length 1529;  
 Best local Similarity 100.0%; Pred. No. 42;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 1111111111  
 Db 133 GLEPPTSG 140

## RESULT 13

S71363  
 Probable ATP-binding cassette transporter ABC-3 - human  
 N:Alternate names: ATP-binding cassette transporter ABC-C  
 C:Species: Homo sapiens (man)  
 C>Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 02-Feb-2001  
 C:Accession: S71363  
 R:Kruppauer, N.; Hofmann, F.; FEBS Lett. 391, 61-65, 1996  
 A:Title: Primary structure of a novel ABC transporter with a chromosomal localization of  
 A:Reference number: S71363; MUID:96326608; PMID:8706931  
 A:Accession: S71363  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1704 <KIU>  
 A:Cross-references: EMBL:X97187; NID:q1514529; PIDN:CA05825.1; PID:e243436; PID:q151453  
 A:Experimental source: cell line medullary thyroid carcinoma  
 C:Genetics:  
 A:Gene: GDB:ABC3  
 A:Cross-references: GDB:3770735; OMIM:601615  
 A:Map position: 16p13.3-16p13.3  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
 C:Keywords: ATP binding; nucleotide binding; P-loop; phosphoprotein; transmembrane prote  
 F:253-283/Domain: transmembrane #status predicted <TM1>  
 F:307-329/Domain: transmembrane #status predicted <TM2>  
 F:345-364/Domain: transmembrane #status predicted <TM3>  
 F:373-394/Domain: transmembrane #status predicted <TM4>  
 F:401-422/Domain: transmembrane #status predicted <TM5>  
 F:432-475/Domain: transmembrane #status predicted <TM6>  
 F:549-739/Domain: ATP-binding cassette homology <ABC1>  
 F:566-573/Region: nucleotide-binding motif A (P-loop)  
 F:685-690/Region: nucleotide-binding motif B  
 F:1100-1110/Domain: transmembrane #status predicted <TM7>  
 F:1145-1169/Domain: transmembrane #status predicted <TM8>  
 F:1181-1207/Domain: transmembrane #status predicted <TM9>  
 F:1215-1236/Domain: transmembrane #status predicted <TM10>  
 F:1245-1264/Domain: transmembrane #status predicted <TM11>

F:1299-1324/Domain: transmembrane #status predicted <TM12>  
 F:1399-1590/Domain: ATP-binding cassette homology <ABC2>  
 F:1416-1423/Region: nucleotide-binding motif A (P-loop)  
 F:1535-1540/Region: nucleotide-binding motif B  
 F:674, 866, 1524/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #  
 F:1344/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status p

Query Match 1.4%; Score 8; DB 2; Length 1704;  
 Best local Similarity 100.0%; Pred. No. 46;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 1111111111  
 Db 581 GLEPPTSG 588

## RESULT 14

A59188  
 ATP-binding cassette transporter ABC3 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 17-May-2002  
 C:Accession: A59188  
 R:Connors, T.D.; Van Raay, T.J.; Petry, L.R.; Klinger, K.W.; Landes, G.M.; Burn, T.C  
 Genomics 39, 231-234, 1997  
 A:Title: The cloning of a human ABC gene (ABC3) mapping to chromosome 16p13.3.  
 A:Reference number: A59188; MUID:97179225; PMID:9027511  
 A:Accession: A59188  
 A>Status: preliminary: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1704 <CONP>  
 A:Cross-references: GB:U78735; NID:q1699037; PIDN:AC050967.1; PID:q1699038  
 C:Genetics:  
 A:Gene: GDB:ABC3  
 A:Cross-references: GDB:3770735; OMIM:601615  
 A:Map position: 16p13.3-16p13.3  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.4%; Score 8; DB 2; Length 1704;  
 Best local Similarity 100.0%; Pred. No. 46;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 1111111111  
 Db 581 GLEPPTSG 588

## RESULT 15

A54774  
 ATP binding cassette transporter ABC1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 05-Apr-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Feb-2001  
 C:Accession: A54774  
 R:Uchiani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimalt, G.  
 Genomics 21, 150-159, 1994  
 A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.  
 A:Reference number: A54774; MUID:94375008; PMID:8068782  
 A:Accession: A54774  
 A:Molecule type: mRNA  
 A:Residues: 1-2201 <KDC>  
 A:Cross-references: GB:X75926; NID:q495256; PIDN:CA033530.1; PID:q495257  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
 C:Keywords: ATP; duplication; nucleotide binding; P-loop  
 F:856-1047/Domain: ATP-binding cassette homology <ABC1>  
 F:873-880/Region: nucleotide-binding motif A (P-loop)  
 F:1869-2060/Domain: ATP-binding cassette homology <ABC2>  
 F:1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 1.4%; Score 8; DB 2; Length 2201;  
 Best local Similarity 100.0%; Pred. No. 58;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 1111111111

Thu Apr 17 07:55:17 2003

us-09-897-778-176.Oligo.rpr

Page 5

Db 888 GLEPPISG 895

Search completed: April 16, 2003, 16:37:37  
Job time : 56.0788 secs

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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:23:10 ; Search time 29.4729 Seconds  
(without alignments)  
814.809 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579  
Sequence: 1 MNKLYIGNLSNAPSDLES.....VKHQOQKALQSGPPQSRK 579

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Swissprot\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.4	84	1 YCX9_OENHO	Q9m6m6 oenothera h
2	8	1.4	311	1 RBFL_MOUSE	P22560 mus musculu
3	8	1.4	997	1 BIRL_SCHPO	O14064 schizosacch
4	8	1.4	1000	1 Y083_CAEEL	P34619 caenorhabdi
5	8	1.4	1704	1 ABC3_HUMAN	O99758 homo sapien
6	8	1.4	2261	1 ABC1_HUMAN	O95477 homo sapien
7	8	1.4	2261	1 ABC1_MOUSE	P41233 mus musculu
8	8	1.4	2434	1 ABC2_HUMAN	P41234 mus musculu
9	8	1.4	2434	1 ABC2_MOUSE	O9bnc7 homo sapien
10	8	1.4	3164	1 TEGU_HSV11	P10220 herpes simp
11	8	1.2	146	1 RL15_BACSU	P19946 bacillus su
12	7	1.2	153	1 HS11_SOYBN	P02519 glycine max
13	7	1.2	183	1 YJGA_ECOLI	P26550 escherichia
14	7	1.2	203	1 CIT1_MOUSE	P97769 mus musculu
15	7	1.2	232	1 YY26_MYCTU	Q50702 mycobacteri
16	7	1.2	239	1 FLA3_METVO	P27805 methanococc
17	7	1.2	285	1 YK62_CAEEL	P45528 caenorhabdi
18	7	1.2	286	1 YRAL_ECOLI	P45528 escherichia
19	7	1.2	291	1 ERA_CAMJE	O9phl1 campylobact
20	7	1.2	299	1 ERA_STAM	O99f59 staphylococ
21	7	1.2	301	1 ERA_AOUAE	O67800 aquifex aeo
22	7	1.2	301	1 ERA_LISIN	O92dp8 listeria in
23	7	1.2	301	1 ERA_LISMO	O8y750 listeria mo
24	7	1.2	302	1 RS3_HAANI	P15009 halobacteri
25	7	1.2	304	1 RS3_HAAMA	P20281 halocaula
26	7	1.2	310	1 YIHG_ECOLI	P32129 escherichia
27	7	1.2	311	1 TUS_YERPE	O916x9 yeastina pe
28	7	1.2	330	1 PDXA_XYLFA	O9p139 xyella fas
29	7	1.2	333	1 TRPD_HAENI	P43858 haemophilus
30	7	1.2	346	1 TERC_ALCSP	P18780 alcaligenes
31	7	1.2	352	1 TERC_SERMA	O52356 serratia ma
32	7	1.2	352	1 RFL_HELPY	P55998 helicobacte
33	7	1.2	355	1 AMPN_ACEPA	Q10736 acetobacter

34	7	1.2	359	1 AROC_CHLPPN	Q9z6m2 chlamydia p
35	7	1.2	367	1 Y001_CAEEL	Q09293 caenorhabdi
36	7	1.2	389	1 NDPE_MOUSE	Q03173 mus musculu
37	7	1.2	399	1 EFTU_PERRIS	O50340 fervidobact
38	7	1.2	431	1 YTG_XYLFA	O9p42 xyella fas
39	7	1.2	449	1 YMG5_CAEEL	O20932 caenorhabdi
40	7	1.2	463	1 ROK_HUMAN	Q07244 homo sapien
41	7	1.2	463	1 ROK_RABIT	O19049 oryctolagus
42	7	1.2	464	1 OTSA_RHISN	P55612 rhizobium s
43	7	1.2	464	1 ROK_MOUSE	O60577 mus musculu
44	7	1.2	484	1 FKHL_YEAST	P40466 saccharomyc
45	7	1.2	486	1 CDSN_HUMAN	Q15517 homo sapien

## ALIGNMENTS

RESULT 1	YCX9_OENHO	STANDARD:	PRT:	84 AA.
AC	Q9MTM6:			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DE	Hypothetical 9.7 kDa protein in trnc-rpob intergenic region (ORF84).			
OS	Oenothera hookeri (Hooker's evening primrose).			
OC	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucosids II; Myrtales; Onagraceae; Oenothera.			
OX	NCBI_TaxID=85636;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Johansen;			
RX	MEDLINE-20309318; PubMed-10852478;			
RA	Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,			
RA	Chiu W.-L., Sears B.;			
RT	"Complete nucleotide sequence of the Oenothera elata plastid			
RT	chromosome, representing plastome I of the five distinguishable			
RT	Euenothera plastomes.";			
RL	Mol. Gen. Genet. 263:581-585(2000).			
CC	-----			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AJ271079; CAB67150.1; "			
KW	Chloroplast; Hypothetical protein.			
SO	SEQUENCE 84 AA; 9674 MW; D37B6A918546E0CB CRC64;			
QY	358 MNLOAHLI 365			
DB	1 MNLOAHLI 8			
QY	358 MNLOAHLI 365			
DB	1 MNLOAHLI 8			
RESULT 2				
RBFL_MOUSE				
ID	P22560:	STANDARD:	PRT:	311 AA.
AC	P22560:			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	IFN-response binding factor 1 (IRBF-1).			
GN	IRBF1.			
OS	Mus musculus (Mouse).			

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Swiss albino;
RX MEDLINE=91095416; Pubmed=1986360;
RA Yan C., Tamm I.;
RT "Molecular cloning and characterization of interferon alpha/beta
RT response element binding factors of the murine (2'-5')oligoadenylate
RT synthetase ME-12 gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:144-148(1991).
CC -1- FUNCTION: BINDS INTERFERON RESPONSE ELEMENTS (IRE).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
CC -----
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CC -----
DR EMBL: M55290; AAA37884.1; -
DR FIR: A38558; A38558.
DR TRANSFAC: T00421; -
DR MGD: MGI:1930074; Irbefl.
KW Phosphorylation; Transcription regulation; DNA-binding;
KM Nuclear protein.
FT SIMILAR 46 83 TO GAL4 DNA-BINDING DOMAIN.
FT DOMAIN 161 184 ASP/GLU-RICH (ACIDIC).
FT MOD.RES 256 270 LEUCINE-ZIPPER.
FT MOD.RES 90 90 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD.RES 247 247 PHOSPHORYLATION (BY CK2) (POTENTIAL).
SQ SEQUENCE 311 AA; 35564 MW; AC45C725162EB03 CRC64;

Query Match 1.4%; Score 8; DB 1; Length 311;
Best local similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NKLIGNL 9
Db 106 NKLIGNL 113

RESULT 3
BIRL SCHPO STANDARD; PRT; 997 AA.
AC 014064;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE BIR1 protein (Chromosome segregation protein cul17).
GN BIR1 OR CUL17 OR PH1 OR SPC92.02C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC NCBI_TaxID=4896;
OX [1]
RP SEQUENCE FROM N.A. FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=21439264; Pubmed=11554922;
RA Yanagishita J., Matsusaka T., Goshima G., Nakamura T., Tatebe H.,
RA Morishita M.;
RT "Bir1/cul17 moving from chromosome to spindle upon the loss of
RT cohesion is required for condensation, spindle elongation and
RT repair.";
RL Genes Cells 6:743-763(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=21848401; Pubmed=11859360;

```

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell J., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger S., Sharp S.,
RA Skellern J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolke G., Yelland G., Aert R., Robben J., Grumppiez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hubert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,
RA Gallé A., Cadieu E., Dreno S., Gloux S., Lelaune V., Mottier S.,
RA Gallé A., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Hochet M., Galliard C., Talada V.A., Garzon A., Rhode G.,
RA Daga R.K., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Kersburg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Sipakovski G.V., Useery D., Barrett B.G., Nurse P.,
RA Nature 415:871-880(2002).
[3]
RA CHARACTERIZATION.
RA MEDLINE=99398681; Pubmed=10468581;
RA Uren A.G., Bellharz T., O'Connell M.J., Bugg S.J., van Driel R.,
RA Vaux D.L., Lithgow T.;
RT "Role for yeast inhibitor of apoptosis (IAP)-like proteins in cell
RT division.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10170-10175(1999).
[4]
RA CHARACTERIZATION.
RA MEDLINE=21850422; Pubmed=11861551;
RA Rajagopalan S., Balasubramanian M.K.;
RT "Schizosaccharomyces pombe Bir1p, a nuclear protein that localizes to
RT kinetochores and the spindle midzone, is essential for chromosome
RT condensation and spindle elongation during mitosis.";
RL Genetics 160:445-456(2002).
[5]
RA FUNCTION.
RA MEDLINE=20035862; Pubmed=10571085;
RA Rajagopalan S., Balasubramanian M.K.;
RT "S. pombe Phl1p, an inhibitor of apoptosis domain containing protein,
RT is essential for chromosome segregation.";
RL FEBS Lett. 460:187-190(1999).
-1- FUNCTION: Seems to act in the pleiotropic control of cell
division. Has a role in chromosome segregation by recruiting
condensin and ark1 kinase to appropriate sites as the cell
progresses through mitosis.
-1- SUBCELLULAR LOCATION: Nuclear. Interacts with the outer
centromeric regions of the chromosomes during interphase. After
chromatid separation, moves to the middle of the spindle.
-1- SIMILARITY: CONTAINS 2 BIR REPEATS.
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CC -----
DR EMBL: AB031034; BA083415.1; -
DR EMBL: AL031323; CAA20434.1; -
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; FALSE_NEG.

```







RX MEDLINE=21157002; PubMed=11257260;  
 RA Bertolini S., Pisciotto L., Seri M., Cusano R., Cantalora A.,  
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.,  
 RT "A point mutation in ABCI gene in a patient with severe premature  
 RT coronary heart disease and mild clinical phenotype of Tangier  
 RT disease.",  
 RL Atherosclerosis 154:599-605(2001).  
 RN [14]  
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.  
 RX MEDLINE=21157003; PubMed=11257261;  
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kietlar D.,  
 RA Probst M., Ordovas J.M., Aslanidis C., Lackner K.J.,  
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,  
 RA Schmitz G.;  
 RT "Common variants in the gene encoding ATP-binding cassette transporter  
 RT 1 in men with low HDL cholesterol levels and coronary heart disease.",  
 RL Atherosclerosis 154:607-611(2001).  
 RN [15]  
 RP VARIANT TD LEU-1506.  
 RX MEDLINE=21369429; PubMed=11476961;  
 RA Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kietlar D., Probst M.,  
 RA Kiec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,  
 RA Sutrop N., Schmitz G.;  
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of  
 RT the ABCA1 gene and its application in genetic analysis of a new  
 RT patient with familial high-density lipoprotein deficiency syndrome.",  
 RL Biochim. Biophys. Acta 1537:42-48(2001).  
 RN [16]  
 RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.  
 RX MEDLINE=21369433; PubMed=11476965;  
 RA Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,  
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;  
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier  
 RT disease and familial high density lipoprotein deficiency with  
 RT coronary heart disease.",  
 RL Biochim. Biophys. Acta 1537:71-78(2001).  
 RN [17]  
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;  
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.  
 RX MEDLINE=21138379; PubMed=11238261;  
 RA Clee S.M., Zwinderman A.H., Engert J.C., Zwarts K.Y.,  
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Miland M., van Dam M.,  
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,  
 RA Hayden M.R.;  
 RT "Common genetic variation in ABCA1 is associated with altered  
 RT lipoprotein levels and a modified risk for coronary artery disease.",  
 RL Circulation 103:1198-1205(2001).  
 RN [18]  
 RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.  
 RX MEDLINE=21645894; PubMed=11785958;  
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,  
 RA Ishihara M., Sakane N., Zhang Z., Tsuji K., Matsuyama A., Ohama T.,  
 RA Matsura F., Ishigami M., Sakai N., Hirooka H., Hattori H.,  
 RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,  
 RA Yanagita S., Matsuzawa Y.;  
 RT "Expression and functional analyses of novel mutations of ATP-binding  
 RT cassette transporter-1 in Japanese patients with high-density  
 RT lipoprotein deficiency.",  
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).  
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION  
 CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL  
 CC TRANSPORT.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN  
 CC MACROPHAGES.  
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
 CC ATP BINDING CASSETTE (ABC) DOMAIN.  
 CC -1- DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN  
 CC DEFICIENCY TYPE I (HDLI), ALSO KNOWN AS TANGIER DISEASE (TD). TD  
 CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY  
 CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,  
 CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY  
 CC DISEASE (CAD).

CC -1- DISEASE: Defects in ABCA1 are a cause of high density lipoprotein  
 Query Match 1.4%; Score 8; DB 1; Length 2261;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 GY 374 GLEPPTSG 381  
 DB 948 GLEPPTSG 955  
 RESULT 7  
 ID ABCI MOUSE STANDARD; PRT; 2261 AA.  
 AC P41233;  
 DT 01-FEB-1995 (rel. 31, Created)  
 DT 16-OCT-2001 (rel. 40, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette  
 DE transporter 1) (ABC-1).  
 GN ABCA1 OR ABC1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DBA/2; TISSUE-Macrophage;  
 RA MEDLINE=94375008; PubMed=8088782;  
 RA Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;  
 RT "Cloning of two novel ABC transporters mapping on human chromosome  
 RT 9.",  
 RL Genomics 21:150-159(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C37BL/6J;  
 RA Qiu Y., Cavelier L., Chiu S., Rubin E., Cheng J.-F.;  
 RT "Human and mouse ABCA1 comparative sequencing and transgenesis studies  
 RT identify potential regulatory sequences.",  
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION  
 CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL  
 CC TRANSPORT (BY SIMILARITY)  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST  
 CC LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.  
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
 CC ATP BINDING CASSETTE (ABC) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.  
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 CC -----  
 DR EMBL: X75926; CAA53530.1; ALT\_INIT.  
 DR EMBL: AF287263; AAG39073.1; ALT\_INIT.  
 DR MGD: MGI:96607; ABCA1.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_Transport.  
 DR Pfam: PF00005; ABC\_tran\_2.  
 DR ProDom: PD000006; ABC\_transportr; 2.  
 DR SMART: SM00382; AAA; 1.  
 DR POSITE: PS00211; ABC\_TRANSPORTER; 1.  
 KM ATP-binding; Glycoprotein; Transmembrane; Transport.  
 FT TRANSMEM 26 42  
 FT TRANSMEM 640 656 POTENTIAL.  
 FT TRANSMEM 690 706 POTENTIAL.  
 FT TRANSMEM 717 733 POTENTIAL.  
 FT TRANSMEM 749 765 POTENTIAL.

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FT TRANSMEM 771 787 POTENTIAL.
FT TRANSMEM 1041 1057 POTENTIAL.
FT TRANSMEM 1351 1367 POTENTIAL.
FT TRANSMEM 1661 1677 POTENTIAL.
FT TRANSMEM 1708 1724 POTENTIAL.
FT TRANSMEM 1737 1753 POTENTIAL.
FT TRANSMEM 1775 1791 POTENTIAL.
FT TRANSMEM 1854 1870 POTENTIAL.
FT NP_BIND 933 940 ATP (POTENTIAL).
FT NP_BIND 1946 1953 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 820 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1144 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1294 1294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1453 1453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1504 1504 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1637 1637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2044 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2238 2238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1567 1568 MISSING (IN REF. 2).
FT CONFLICT 2024 2024 MISSING (IN REF. 2).
SQ SEQUENCE 2261 AA; 254011 MW; FA62B21FD1D09F9 CRC64;

Query Match 1.4%; Score 8; DB 1; Length 2261;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381
Db 948 GLEPPTSG 955

RESULT 8
ABC2_MOUSE STANDARD; PRT; 2434 AA.
ID ABC2_MOUSE
AC P41234;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 2 (ATP-binding cassette transporter 2) (ATP-binding cassette 2).
GN ABCA2 OR ABC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND REVISIONS.
RC STRAIN-DBA/2;
RA Chimini G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBD databases.
RN [2]
RP SEQUENCE OF 964-2434 FROM N.A.
RC STRAIN-DBA/2; TISSUE-Macrophage;
RX MEDLINE=94375008; PubMed=8088782;
RA Luciani M.F., Denzot F., Savary S., Mattei M.-G., Chimini G.;
RT *Cloning of two novel ABC transporters mapping on human chromosome 9.
RT Genomics 21:150-159(1994).
CC -!- FUNCTION: PROBABLE TRANSPORTER, ITS NATURAL SUBSTRATE HAS NOT BEEN

```

```

CC CC FOUND YET. MAY HAVE A ROLE IN MACROPHAGE LIPID METABOLISM AND
CC CC NEURAL DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC LEVELS ARE FOUND IN BRAIN AND PREGNANT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X75827; CAA3531.2; -
DR MGI: 99606; Abca2.
DR InterPro: IPR003593; AAA-ATPase.
DR InterPro: IPR003439; ABC-transporter.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC-transporter; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC-TRANSPORTER; 1.
DR ATP-binding; Transport; Transmembrane; Repeat; Glycoprotein.
KW TRANSMEM 21
FT TRANSMEM 705 727 POTENTIAL.
FT TRANSMEM 748 770 POTENTIAL.
FT TRANSMEM 780 802 POTENTIAL.
FT TRANSMEM 809 831 POTENTIAL.
FT TRANSMEM 1793 1815 POTENTIAL.
FT TRANSMEM 1846 1865 POTENTIAL.
FT TRANSMEM 1875 1897 POTENTIAL.
FT TRANSMEM 1904 1926 POTENTIAL.
FT NP_BIND 1024 1031 ATP (POTENTIAL).
FT NP_BIND 2088 2095 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 589 589 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 599 599 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1408 1408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1496 1496 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1549 1549 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1557 1557 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1776 1776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2055 2055 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2434 AA; 270582 MW; 3CEDD48ED5692005 CRC64;

Query Match 1.4%; Score 8; DB 1; Length 2434;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381
Db 1039 GLEPPTSG 1046

RESULT 9
ABC2_HUMAN

```



DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE Large tegument protein (Virion protein UL36).  
 GN UL36.  
 OS Herpes simplex virus (type 1 / strain 17).  
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=86274327; PubMed=2839594;  
 RA McGeoch D.J., Daillymple M.A., Davison A.J., Dolan A., Frame M.C.,  
 RA McNab D., Perry L.J., Scott J.E., Taylor P.;  
 RT The complete DNA sequence of the long unique region in the genome of  
 RT herpes simplex virus type 1.;  
 RL J. Gen. Virol. 69:1531-1574(1988).  
 CC -1- FUNCTION: TEGUMENT PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,  
 CC EHV-1 24, BBV BPFL1, HVS-1 64, VZV 22, AND HCMV UL48.  
 CC -----  
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 CC -----  
 DR EMBL: X14112; CAA32311.1;  
 DR PIR: I30085; WHEHE6.  
 DR InterPro: IPR005210; Herpes\_UL36.  
 DR Pfam: PF03586; Herpes\_UL36; 1.  
 KM Repeat.  
 FT DOMAIN 2911 2960 35 X 2 AA TANDEM REPEATS OF P-Q.  
 SO SEQUENCE 3164 AA; 335857 MW; CC5D31FF4F9FE3FA CRC64;  
 QY 383 PPSTGPP 390 1.4%; Score 8; DB 1; Length 3164;  
 DB 2857 PPSTGPP 2864 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query Match  
 1.4%; Score 8; DB 1; Length 3164;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 11  
 ID RL15\_BACSU STANDARD; PRT: 146 AA.  
 AC P19946;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein L15.  
 GN RPL0.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90292990; PubMed=2113521;  
 RA Nakamura K., Nakamura A., Takematsu H., Yoshikawa H., Yamane K.;  
 RT Cloning and characterization of a Bacillus subtilis gene homologous  
 RT to E. coli secY.;  
 RL J. Biochem. 107:603-607(1990).  
 CC [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=90221911; PubMed=2139212;  
 RA Yoshikawa H., Doi R.H.;  
 RT "Sequence of the Bacillus subtilis spectinomycin resistance gene  
 RT region".  
 RL Nucleic Acids Res. 18:1647-1647(1990).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / Marburg;  
 RX MEDLINE=96186897; PubMed=8635744;  
 RT Suh J.-W., Boylan S.A., Oh S.H., Price C.W.;  
 RT Genetic and transcriptional organization of the Bacillus subtilis  
 RT spc-alpha region.;  
 RL Gene 169:17-23(1996).  
 CC [4]  
 RN SEQUENCE OF 94-146 FROM N.A.  
 RP STRAIN-168;  
 RX MEDLINE=90251170; PubMed=2110998;  
 RA Suh J.-W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,  
 RA Price C.W.;  
 RT "Isolation of a secY homologue from Bacillus subtilis: evidence for a  
 RT common protein export pathway in eubacteria".  
 RL Mol. Microbiol. 4:305-314(1990).  
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL: D00619; BAA00494.1;  
 DR EMBL: X51329; CAA35711.1;  
 DR EMBL: L47971; AAB06818.1;  
 DR EMBL: M31102; AAB59117.1;  
 DR EMBL: Z99104; CAB11911.1;  
 DR PIR: S12682; RSBSU5.  
 DR Subtilist; BG10444; RPL0.  
 DR InterPro: IPR001196; Ribosomal\_L15.  
 DR Pfam: PF00256; L15; 1.  
 DR TIGRfam: TIGR01071; RPL0\_bact; 1.  
 DR PROSITE: PS00475; RIBOSOMAL\_L15; 1.  
 KM Ribosomal protein; rRNA-binding; Complete proteome.  
 SO SEQUENCE 146 AA; 15363 MW; 5DB07A902B26C11 CRC64;  
 QY 136 LDKLNGF 142 1.2%; Score 7; DB 1; Length 146;  
 DB 79 LDKLNGF 85 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query Match  
 1.2%; Score 7; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 12  
 ID HS11\_SOYBN STANDARD; PRT: 153 AA.  
 AC P02519;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE 17.3 kDa class I heat shock protein (HSP 17.3).  
 GN HSP17.3-B OR HS6871.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schoffl F., Raschke E., Nagao R.T.;  
 RT "The DNA sequence analysis of soybean heat-shock genes and  
 RT identification of possible regulatory promoter elements".  
 RL EMBO J. 3:2491-2497(1984).  
 CC -1- SUBUNIT: FORMS OLIGOMERIC STRUCTURES.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

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CC -1 SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
CC PARTLY.
CC -1 SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20. CLASS I AND II
CC WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
CC AND CLASS IV WHICH IS IN THE ENOMEMBRANE. THIS PROTEIN BELONGS
CC TO CLASS I.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: X01104; CAA25578.1; -
CC PIR: A02922; HHSY17.
CC InterPro: IPR002068; Hsp20.
CC Pfam: PF00011; HSP20_1.
CC PROSITE: PS01031; HSP20_1.
CC Heat shock; Multigene family.
CC KW SEQUENCE 153 AA; 17347 MW; A1A8612B9EC86819 CRC64;
SQ
Query Match 1.2%; Score 7; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 483 KEEVKLE 489
| | | | |
DB 68 KEEVKLE 74
-----
RESULT 13
YUGA_ECOLI STANDARD: PRT; 183 AA.
ID YUGA_ECOLI
AC P26650;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yj9A (Y96 protein).
GN YUGA OR X96 OR B4234 OR Z5844 OR ECS5211.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RA Rodriguez-Sainz M.C., Moreno F.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=96177756; PubMed=8604133;
RA Moriyama N., Shimizu H., Takiguchi S., Baba Y., Amino H.,
RA Horinouchi T., Sekimizu K., Miki T.;
RT "Evidence for involvement of Escherichia coli genes pmhA, csrA and a
RT previously unrecognized gene tldD, in the control of DNA gyrase by
RT lsdC (ccdB) of sex factor F.'";
RL J. Mol. Biol. 256:483-502(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RC MEDLINE=21074935; PubMed=11206551;

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RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1 SIMILARITY: STRONG. TO H. INFLUENZAE H1151.
-----
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-----
CC EMBL: M95096; AAA24760.1; -
CC EMBL: U14003; AAA97131.1; -
CC EMBL: AE000494; AAC77191.1; -
CC EMBL: D44452; BAA07914.1; -
CC EMBL: AE005655; AAG59431.1; -
CC EMBL: AP002568; BAB38634.1; -
CC Ecogene: EG11410; yj9A.
KM Hypothetical protein; Complete proteome.
FT DOMAIN 15 23 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 183 AA; 21359 MW; 069CF47719CD59CB CRC64;
Query Match 1.2%; Score 7; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 133 RQALDKL 139
| | | | |
DB 98 RQALDKL 104
-----
RESULT 14
CIT1_MOUSE STANDARD: PRT; 203 AA.
ID CIT1_MOUSE
AC P97769;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cbp/p300-Interacting transactivator 1 (Melanocyte-specific protein 1).
GN CITFD1 OR MS21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97057236; PubMed=8901575;
RA Shida T., Fenner M.H., Isselbacher K.J.;
RT "msg1, a novel melanocyte-specific gene, encodes a nuclear protein
RT and is associated with pigmentation.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12298-12303(1996).
CC -1 FUNCTION: NOT KNOWN. SEEMS TO BE ASSOCIATED WITH PIGMENTATION.
CC -1 SUBCELLULAR LOCATION: Nuclear.
CC -1 TISSUE SPECIFICITY: EXPRESSED ONLY IN MELANOCYTES AND TESTIS.
CC EXPRESSED AT HIGH LEVELS IN THE STRONGLY PIGMENTED MELANOMA CELLS

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CC      BUT AT LOW LEVELS IN THE WEAKLY PIGMENTED CELLS.
CC      -1- SIMILARITY: BELONGS TO THE CITED FAMILY.
CC      -----
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CC      -----
CC      EMBL: U65091; AAC31048.1;
CC      D8      MCD: MCD:108023; Cited1.
CC      KM      Nucleic Protein:
CC      PT      DOMAIN 159
CC      SEQUENCE 203 AA: 20800 MW; BE968A5182873003 CRC64;
CC
CC      Query Match
CC      Best Local Similarity 100.0%; Score 7; DB 1; Length 203;
CC      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
OY      183 GSPGSVS 189
DB      141 GSPGSVS 147

RESULT 15
YY26_MYCTU STANDARD: PRT: 232 AA.
AC      050702:
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical PPE-family protein RV3426.
GN      RV3426 OR MTCY78.03C.
OS      Mycobacterium tuberculosis.
OC      Bacteria; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX      NCBI_Taxid:1773;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-H37RV;
RX      MEDLINE-98295987; PubMed-9634230;
RA      Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA      Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA      Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA      Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA      Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA      Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA      Rulston J.E., Taylor K., Whitehead S., Squares S., Squares R.,
RA      Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT      "Deciphering the biology of Mycobacterium tuberculosis from the
RT      complete genome sequence.";
RL      Nature 393:537-544(1998).
CC      -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
CC      -----
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CC      -----
CC      EMBL: Z77165; CAB01030.1;
CC      DR      Tuberculist; RV3426;
CC      DR      InterPro: IPR000030; Microbac_PPE.
CC      DR      Pfam: PF00823; PPE; 1.
CC      KW      Hypothetical protein; Complete proteome.
CC      SEQUENCE 232 AA: 25872 MW; D76512D49EB272C6 CRC64;
CC
CC      Query Match
CC      Best Local Similarity 100.0%; Score 7; DB 1; Length 232;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      168 PRGRRL 174
DB      179 PRGRRL 185
Search completed: April 16, 2003, 16:35:19
Job time : 37.4729 secs

```

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:30:00 ; Search time 70.3547 Seconds  
(without alignments)  
1695.712 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579  
Sequence: 1 MNKLYIGNLSENAPSDLES.....VKHQQQKALQSGPQSRK 579

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archae:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	579	4 O00425	O00425 homo sapien
2	104	18.0	579	11 O9GPN8	O9GPN8 mus musculu
3	45	7.8	533	13 O57526	O57526 xenopus lae
4	45	7.8	534	13 O73932	O73932 xenopus lae
5	43	7.4	582	13 O9FW80	O9FW80 brachydiano
6	36	6.2	576	13 O42254	O42254 gallus gall
7	36	6.2	577	4 O9N218	O9N218 homo sapien
8	36	6.2	577	11 O88477	O88477 mus musculu
9	27	4.7	100	11 O9D054	O9D054 mus musculu
10	19	3.3	556	4 O9Y6M1	O9Y6M1 homo sapien
11	11	1.4	84	8 O9MTM6	O9MTM6 oenothera h
12	8	1.4	142	17 O8TXJ1	O8TXJ1 methanopyru
13	8	1.4	152	5 O9BIJ0	O9BIJ0 patella vul
14	8	1.4	242	16 O97K26	O97K26 clostridium
15	8	1.4	318	10 O9S827	O9S827 scutellaria
16	8	1.4	324	16 O8X107	O8X107 yerstinia pe

17	8	1.4	338	16 O930F4	O930F4 rhizobium m
18	8	1.4	441	17 O9HIW6	O9HIW6 thermoplasm
19	8	1.4	558	5 O9VZ69	O9VZ69 drosophila
20	8	1.4	566	5 O9NCS9	O9NCS9 drosophila
21	8	1.4	640	10 O9ASX3	O9ASX3 arabidopsis
22	8	1.4	644	10 O9FNK3	O9FNK3 zymomonas m
23	8	1.4	762	2 O9EZ93	O9EZ93 arabidopsis
24	8	1.4	829	16 O9BDP8	O9BDP8 rhizobium 1
25	8	1.4	925	5 O25342	O25342 leishmania
26	8	1.4	1101	16 O53347	O53347 mycobacteri
27	8	1.4	1220	5 O17832	O17832 caenorhanti
28	8	1.4	1529	4 O9UPU0	O9UPU0 homo sapien
29	8	1.4	1704	11 O8R420	O8R420 mus musculu
30	8	1.4	1944	3 O9UVL8	O9UVL8 pneumocysti
31	8	1.4	1944	3 O9HEZ4	O9HEZ4 pneumocysti
32	8	1.4	1952	5 O95SN5	O95SN5 drosophila
33	8	1.4	2260	13 O8UVV4	O8UVV4 gallus gall
34	8	1.4	2434	11 O9ESR9	O9ESR9 rattus norv
35	8	1.4	2436	4 O9HC28	O9HC28 homo sapien
36	8	1.4	3164	12 O69088	O69088 human herpe
37	8	1.4	4547	5 O9W343	O9W343 drosophila
38	7	1.2	59	17 O9HRB8	O9HRB8 halobacteri
39	7	1.2	62	9 O9B047	O9B047 mycobacteri
40	7	1.2	76	16 O8YWU2	O8YWU2 anabaena sp
41	7	1.2	84	12 O36987	O36987 newcastle d
42	7	1.2	84	12 O36989	O36989 newcastle d
43	7	1.2	84	12 O36991	O36991 newcastle d
44	7	1.2	84	12 O36997	O36997 newcastle d
45	7	1.2	84	12 O37001	O37001 newcastle d

## ALIGNMENTS

RESULT 1	ID	AC	000425	PRELIMINARY	PRT:	579 AA.
AC	000425	01-JUL-1997 (TREMBLrel. 04, Created)				
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	Putative RNA binding protein KOC (KOC).					
GN	KOC.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_Taxid=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Mueller-Pillasch F., Lacher U., Wallrapp C., Et AL.;					
RL	Oncogene 0:0-0(0).					
RN	(2)					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=PANCREAS;					
RA	Mueller-Pillasch F., Lacher U., Wallrapp C.;					
RL	Submitted (OCR-1996) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: U97188; AAC35208.1; -					
DR	EMBL: U76705; AAD09223.1; -					
DR	InterPro: IPR004087; KH_dom.					
DR	InterPro: IPR004088; KH_type_1.					
DR	InterPro: IPR005054; RNA_rec_mot.					
DR	Pfam: PF00013; KH_domain; 4.					
DR	Pfam: PF00076; rrm; 2.					
DR	SMART: SM00322; KH; 4.					
DR	SMART: SM00360; RRM; 2.					
DR	PROSITE: PS50084; KH_TYPE_1; 4.					
DR	PROSITE: PS50102; RRM; 2.					
DR	PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.					
SQ	SEQUENCE 579 AA: 63720 MW; AE5C3A8EE3C135C5 CRC64;					
Query Match	100.0%; Score 579; DB 4; Length 579;					
Best Local Similarity	100.0%; Pred. No. 0;					
Matches	579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

Qy	1	MLKLTIGLSNMAAPDSEITFKMA PVSGPFLYTGK VVDDPDSMAKATIALSGK	60
Dd	1	MKKLTIGLSNMAAPDSEITFKMAKIPVSGPFLYTGKAVDDPDSMAKATIALSGK	60
Qy	61	IEHKKP1EVEHSPKROB1IKRLQ1RNI1PH1LQWELDLSLVOYGVSEEDVYNDSETA	120
Dd	61	IEHKKP1EVEHSPKROB1IKRLQ1RNI1PH1LQWELDLSLVOYGVSEEDVYNDSETA	120
Qy	121	VNNVTSKSDARQALDKINGOLENTFLKVAIT1PDMAAQON1LOOPGRKRGLORSS	180
Dd	121	VNNVTSKSDARQALDKINGOLENTFLKVAIT1PDMAAQON1LOOPGRKRGLORSS	180
Qy	181	ROGSVGSYKSKRPCDLP1PLKLP1PO1PVGA1ITGEGAT1RNT1KOTOSK1DVHKKEMAGAA	240
Dd	181	ROGSVGSYKSKRPCDLP1PLKLP1PO1PVGA1ITGEGAT1RNT1KOTOSK1DVHKKEMAGAA	240
Qy	241	EKST1LTSPGGS1SAACKS1ET1MHKEAD1KTTEE1PK1L1ANN1VGL1IGKEGRNLK	300
Dd	241	EKST1LTSPGGS1SAACKS1ET1MHKEAD1KTTEE1PK1L1ANN1VGL1IGKEGRNLK	300
Qy	301	K1EODTOK1T1IS1LOEL1TLV1PERT1TVKGN1ETCAKAE1MKK1RESYENDIASMNL	360
Dd	301	K1EODTOK1T1IS1LOEL1TLV1PERT1TVKGN1ETCAKAE1MKK1RESYENDIASMNL	360
Qy	361	QAH1L1PG1NLNA1GLP1PTSGMP1PTSGPSPASMT1PYP1QDQSETEFVH1Q1PALSVAI	420
Dd	361	QAH1L1PG1NLNA1GLP1PTSGMP1PTSGPSPASMT1PYP1QDQSETEFVH1Q1PALSVAI	420
Qy	421	ICKOGOH1KOL1SRFAGAS1K1IAPAPADPAV1RNV1IT1GPEAOE1KAG1RYG1K1EENFV	480
Dd	421	ICKOGOH1KOL1SRFAGAS1K1IAPAPADPAV1RNV1IT1GPEAOE1KAG1RYG1K1EENFV	480
Qy	481	SRKEEVLK1EAH1IRP1SFAAG1RY1IGKGG1TVNEL1ONLSA1EYV1ERD1OTDPEND1OVV1IT	540
Dd	481	SRKEEVLK1EAH1IRP1SFAAG1RY1IGKGG1TVNEL1ONLSA1EYV1ERD1OTDPEND1OVV1IT	540
Qy	541	GHFYACQV1AOK1T1OEL1IT1OVK1HOQ1AAL1OSGP1SRRK	579
Dd	541	GHFYACQV1AOK1T1OEL1IT1OVK1HOQ1AAL1OSGP1SRRK	579

RESULT 2	PRELIMINARY:	PRT:	579 AA.
09CPENB8			
AC	09CPENB8		
DT	01-JUN-2001 (TREMblref. 17, Created)		
DT	01-JUN-2001 (TREMblref. 17, Last sequence update)		
DT	01-JUN-2002 (TREMblref. 21, Last annotation update)		
DE	10 days embryo cDNA, RIKEN full-length enriched library,		
DE	clone:2610036B18, full insert sequence (1qf2 mRNA-binding protein		
DE	3)		
GN	1qf2BP3 OR 2610101N1R1R OR MIM33.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NC	NCBI_TaxId:10090;		
RN	11		
RP	SEQUENCE FROM N.A.		
RC	STRAIN:C57BL/6J TISSUE:EMBryo;		
RC	MEDLINE:21083660; PubMed:11217851;		
RA	Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hata A., Fukunishi Y., Kono H., Adachi T., Fukuda S.,		
RA	Aizawa K., Iwaza M., Gishi K., Kiyosawa H., Kondo S., Yamana K I.,		
RA	Salto T., Ozawa Y., Nishikori T., Bono H., Kusakawa T., Salto R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batloy B., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,		
RA	Kuhen P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Sakaki K., Okfido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J. D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Gustromstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gastinichin S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyokura K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsunki S.,  
 RA Hashizaki Y.,  
 RT "functional annotation of a full-length mouse cDNA collection.,"  
 RL Nature 409:685-690(2001).  
 RN [2]  
 RP  
 RP SEQUENCE FROM N.A.  
 RA Mori H., Sakakibara S., Imai T., Nakamura Y., Iijima T., Suzuki A.,  
 RA Yasui H., Takeda M., Okano H.,  
 RT "expression of mouse igf2 mRNA-binding protein 3 and its implications  
 for the developing central nervous system.,"  
 RL J. Neurosci. Res. 0:0-0(2001).  
 DR EMBL: AK011689; BAB27779.1; -  
 DR EMBL: AB046173; BAB19755.1; -  
 DR MGD: MGI:1890359; Igf2bp3.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR000504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PS50084; KH\_type\_1; 4.  
 DR PROSITE: PS50102; RRM; 2.  
 QO SOURCE 579 AA; 63574 MW; CABD9AA35B39287 CRC64;

[illegible]



DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 593 AA; 65385 MW; 5A5AE4B4A1D55DF7 CRC64;

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 KTEEIPKILAHNNFVGRLLGKGRNKKTEQDTFKITISPLQ 316  
 Db 281 KTEEIPKILAHNNFVGRLLGKGRNKKTEQDTFKITISPLQ 325

## RESULT 4

073932 PRELIMINARY; PRT; 594 AA.  
 AC 073932;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Vg1 RNA binding protein variant D.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NC NCBL\_TaxID=8355;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA Havin L., Gilt A., Elisha Z., Oberman F., Yaniv K.,  
 RA Pressman Schwartz S., Standard N.M., Yisraeli J.K.;  
 RL Genes Dev. 0:0-0(1998).  
 RN 12

RP SEQUENCE FROM N.A.  
 RX MEDLINE-98228351; PubMed-9560341;  
 RA Deslier J.O., Highett M.I., Abramson T., Schnapp B.J.;  
 RT "A highly conserved RNA-binding protein for cytoplasmic mRNA  
 RT localization in vertebrates";  
 RL Curr. Biol. 8:489-496(1998).  
 DR EMBL: AF064634; AAC18598.1; -.  
 DR EMBL: AF055923; AAC41285.1; -.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 594 AA; 65643 MW; 5ACEN7BFF0856DD6 CRC64;

Query Match  
 Best Local Similarity 7.8%; Score 45; DB 13; Length 594;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 KTEEIPKILAHNNFVGRLLGKGRNKKTEQDTFKITISPLQ 316  
 Db 282 KTEEIPKILAHNNFVGRLLGKGRNKKTEQDTFKITISPLQ 326

## RESULT 5

09PW80 PRELIMINARY; PRT; 582 AA.  
 AC 09PW80;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Vg1 RNA binding protein.  
 GN DVRIKBP.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBL\_TaxID=7955;  
 RN 111  
 RP SEQUENCE FROM N.A.

RA Zhang Q., Yaniv K., Oberman F., Wolke U., Gilt A., Fromer M.,  
 RA Taylor W., Meyer D., Standard N., Raz E., Yisraeli J.K.;  
 RT "Vg1 RBP intracellular distribution and evolutionarily conserved  
 RT expression suggest multiple roles during development";  
 RL Mech. Dev. 0:0-0(1999).  
 DR EMBL: AF161270; AAD45610.1; -.  
 DR ZFIN: ZDB-GENE-000308-1; dvrlbp.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 SO SEQUENCE 582 AA; 63351 MW; 9DAE63200681B306 CRC64;

Query Match  
 Best Local Similarity 7.4%; Score 43; DB 13; Length 582;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 TEIEIPKILAHNNFVGRLLGKGRNKKTEQDTFKITISPLQ 316  
 Db 273 TEIEIPKILAHNNFVGRLLGKGRNKKTEQDTFKITISPLQ 315

## RESULT 6

042254 PRELIMINARY; PRT; 576 AA.  
 AC 042254;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Zipcode binding protein.  
 GN ZBP1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NC NCBL\_TaxID=9031;  
 RN 111  
 RP SEQUENCE FROM N.A.

RX MEDLINE-97220077; PubMed-9121465;  
 RA Ross A.F., Oleynikov Y.S., Kislauskis E.H., Tanaja K.L., Singer R.H.;  
 RT "Characterization of a beta-actin mRNA zipcode-binding protein";  
 RL Mol. Cell. Biol. 17:2158-2165(1997).  
 DR EMBL: AF026527; AAB82299.1; -.

DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 576 AA; 63271 MW; 01AAE2D1D81C8811 CRC64;

Query Match  
 Best Local Similarity 6.2%; Score 36; DB 13; Length 576;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 VGAIIGKCATIRNITKOTOSKIDVHRKKNAGAAR 242
    |||||||||||||||||||||||||||||||||||
DB 207 VGAIIGKCATIRNITKOTOSKIDVHRKKNAGAAR 242

RESULT 7
OQNZ18 PRELIMINARY: PRT: 577 AA.
AC OQNZ18:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE mRNA-binding protein CRDBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ioannidis P., Trangas T., Dimitriadis E., Samiotaki M.,
RA Panousakopoulos G., Kyriazoglou I., Voutoulas S., Tsipalis C.M.,
RA Kiltas C., Aganitis N., Pandis N.;
RT Ectopic expression of a KH-domain containing protein, highly
RT homologous to both human IMP-1 and mouse CRD-BP, in benign and
RT malignant mesenchymal tumors.
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF198254; AAF37203.1;
DR HSSP: P11940; ICVJ.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR004088; KH_type_1.
DR InterPro: IPR005054; RNA_rec_mot.
DR Pfam: PF00013; KH-domain; 4.
DR Pfam: PF00076; rtm; 2.
DR SMART: SM00322; KH; 4.
DR SMART: SM00360; RRM; 2.
DR PROSITE: PS50084; KH_type_1; 4.
DR PROSITE: PS50102; RRM; 2.
SQ SEQUENCE 577 AA; 63456 MW; 0749A060F252D81D CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 4; Length 577;
Pred. No. 1.le-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 VGAIIGKCATIRNITKOTOSKIDVHRKKNAGAAR 242
    |||||||||||||||||||||||||||||||||||
DB 207 VGAIIGKCATIRNITKOTOSKIDVHRKKNAGAAR 242

RESULT 8
OQNZ18 PRELIMINARY: PRT: 577 AA.
AC OQNZ18:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coding region determinant binding protein (Coding region determinant-
DE binding protein).
DE Ige2Bp1 OR CRDBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92217743; PubMed=1559612;
RA Bernstein P.L., Herrick D.J., Prokipcak R.D., Ross J.;
RT Control of c-myc mRNA half-life in vitro by a protein capable of
RT binding to a coding region stability determinant.
RL Genes Dev. 6:642-654(1992).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE=94158886; PubMed=8114742;
RA Herrick D.J., Ross J.;
RT "The half-life of c-myc mRNA in growing and serum-stimulated cells:
RT influence of the coding and 3' untranslated regions and role of
RT ribosome translocation."
RL Mol. Cell. Biol. 14:2119-2128(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=94179348; PubMed=8132663;
RA Prokipcak R.D., Herrick D.J., Ross J.;
RT Purification and properties of a protein that binds to the C-terminal
RT coding region of human c-myc mRNA.
RL J. Biol. Chem. 269:9261-9269(1994).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=97322234; PubMed=9178888;
RA Leeds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.;
RA Gruppiso P.A., Ross J.;
RT "Developmental regulation of CRD-BP, an RNA-binding protein that
RT stabilizes c-myc mRNA in vitro."
RL Oncogene 14:1279-1286(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ross J., Prokipcak R.D., Leeds P., Doyle G.A.R., Betz N.A.,
RA Fleisig A.J.;
RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Funada S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gajobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boftelli D., Bojunga N., Aono H., Baldarelli R., Barsh G.,
RA Gustincich S., Hill D., Hofmann M., Carninci P., de Bonaldo M.F.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshew-Borris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RX EMBL: AF061569; AAC72743.1;
DR EMBL: AK013940; BAB29071.1;
DR HSSP: P11940; ICVJ.
DR MGD: MGI:1890357; Ige2Bp1.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR004088; KH_type_1.
DR InterPro: IPR005054; RNA_rec_mot.
DR Pfam: PF00013; KH-domain; 4.
DR Pfam: PF00076; rtm; 2.
DR SMART: SM00322; KH; 4.
DR SMART: SM00360; RRM; 2.
DR PROSITE: PS50084; KH_type_1; 4.
DR PROSITE: PS50102; RRM; 2.
SQ SEQUENCE 577 AA; 63450 MW; EFB1AF2F9F0344 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 11; Length 577;
Pred. No. 1.le-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 VGAIIGKCATIRNITKOTOSKIDVHRKKNAGAAR 242
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DB 207 VGAIIGKCATIRNITKOTOSKIDVHRKKNAGAAR 242

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[illegible]

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RP SEQUENCE FROM N.A.
RC STRAIN-AV19 / DSM 6324 / JCM 9639;
RX MEDLINE-21927647; PubMed-11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravid L.,
RA Nalekh A.G., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
RW EMBL: AE010361; AAM01897.1;
KW Elongation factor; Complete proteome.
SQ SEQUENCE 142 AA; 15909 MW; BF4FEFC4E03B2677 CRC64;

Query Match 1.4%; Score 8; DB 17; Length 142;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 GRVYKGG 507
Db 113 GRVYKGG 120

RESULT 13
ID 09BIJ0 PRELIMINARY; PRT: 152 AA.
AC 09BIJ0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative RNA-binding protein (Fragment).
OS Patella vulgata (Common limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Patelioidae; Patelidae; Patella.
OX NCBI_TaxID=6465;
RN [1]
RP SEQUENCE FROM N.A.
RA Klerkx A.H.E.M., de Boer E., van Loon A.E.;
RT "Spatio-temporal expression of a gene encoding a putative RNA-binding
RT protein during the early larval development of the mollusc Patella
RT vulgata."
RL Dev. Genes Evol. 0:0-0(2001).
RW EMBL: AF61436; AAK32728.1;
DR InterPro: IPR002952; Eggshell.
DR InterPro: IPR004087; KH_dom.
DR Pfam: PF00013; KH-domain_1.
DR PRINTS: PR01228; EGGSHELL.
DR SMART: SM00322; KH.1.
DR PROSITE: PS0084; KH_TYPE_1; 1.
FT NON_TER 1
SQ SEQUENCE 152 AA; 15181 MW; 2950AB44E4754F97 CRC64;

Query Match 1.4%; Score 8; DB 5; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 GRVYKGG 507
Db 42 GRVYKGG 49

RESULT 14
ID 097KZ6 PRELIMINARY; PRT: 242 AA.
AC 097KZ6;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glycerol uptake facilitator protein, permease.
CN CAC0770
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

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OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE-21359325; PubMed-1146286;
RA Nieling J., Bleton G., Ometchenko M.V., Makarova K.S., Zeng O.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
RA Benmet G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
RW EMBL: AE007592; AAK78746.1;
DR InterPro: IPR000425; MIP_family.
DR Pfam: PF00230; MIP.1.
DR PRINTS: PR00783; MINTINSICP.
DR PRODOM: PD000295; MIP_family.1.
DR PROSITE: PS00221; MIP; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 25807 MW; 26E7A62AE7377AF CRC64;

Query Match 1.4%; Score 8; DB 16; Length 242;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 QFVGAIIG 212
Db 94 QFVGAIIG 101

RESULT 15
ID 09SSZ7 PRELIMINARY; PRT: 318 AA.
AC 09SSZ7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Peroxidase 3.
OS Scutellaria baicalensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteroideae; eusterids I; Lamiales; Lamnaceae; Scutellaria.
OX NCBI_TaxID=65409;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-94403061; PubMed-10473572;
RA Morimoto S., Tateishi N., Inuyama M., Tanaka F., Tanaka H., Shoyama Y.;
RT "Identification and molecular characterization of novel peroxidase
RT with structural protein-like properties."
RL J. Biol. Chem. 274:26192-26198(1999).
RW EMBL: AB024439; BAA73789.1;
DR HSSP: P22195; ISCH.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase.1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
SQ SEQUENCE 318 AA; 33903 MW; 6CDD0DA3FE470C83 CRC64;

Query Match 1.4%; Score 8; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 PGILNAL 373
Db 165 PGILNAL 172

Search completed: April 16, 2003, 16:36:37
Job time : 74.3547 secs

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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:18:40 ; Search time 32.3251 Seconds

(without alignments)  
527.016 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 2956  
Sequence: 1 MNKLYIGNLSNNAAPSDLES.....VKOHQOKALQSGPPOSRRK 579

Scoring table:  
BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA: \*  
2: /cgn2\_6/prodata1/1/aa/5A.COMB.pep: \*  
3: /cgn2\_6/prodata1/1/aa/5B.COMB.pep: \*  
4: /cgn2\_6/prodata1/1/aa/5C.COMB.pep: \*  
5: /cgn2\_6/prodata1/1/aa/5D.COMB.pep: \*  
6: /cgn2\_6/prodata1/1/aa/5E.COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2956	100.0	579	4 US-09-643-597-176	Sequence 176, App
2	2943	99.6	579	4 US-09-643-597-348	Sequence 348, App
3	2190	74.1	577	4 US-09-261-855-2	Sequence 2, App11
4	241	8.2	644	1 US-08-021-608D-2	Sequence 2, App11
5	241	8.2	644	1 US-08-726-160-2	Sequence 2, App11
6	241	8.2	644	5 PCT-US94-01782-2	Sequence 2, App11
7	238	8.1	49	4 US-09-261-855-22	Sequence 22, App1
8	227	8.0	48	4 US-09-261-855-24	Sequence 24, App1
9	236.5	8.0	643	1 US-08-021-608D-10	Sequence 10, App1
10	236.5	8.0	643	1 US-08-726-160-10	Sequence 10, App1
11	236.5	8.0	643	5 PCT-US94-01782-10	Sequence 10, App1
12	232	7.8	49	4 US-09-261-855-18	Sequence 18, App1
13	229.5	7.8	590	1 US-08-021-608D-8	Sequence 8, App11
14	229.5	7.8	590	1 US-08-726-160-8	Sequence 8, App11
15	229.5	7.8	590	5 PCT-US94-01782-8	Sequence 8, App11
16	227	7.7	47	4 US-09-261-855-23	Sequence 23, App1
17	227	7.7	530	4 US-08-187-793-4	Sequence 4, App11
18	225	7.6	47	4 US-09-261-855-21	Sequence 21, App1
19	219	7.4	48	4 US-09-261-855-20	Sequence 20, App1
20	218	7.4	47	4 US-09-261-855-17	Sequence 17, App1
21	190	6.4	47	4 US-09-261-855-19	Sequence 19, App1
22	159.5	5.4	471	4 US-08-866-928B-1	Sequence 1, App11
23	154	5.2	343	1 US-08-187-793-2	Sequence 2, App11
24	147	5.0	243	1 US-08-021-608D-6	Sequence 6, App11
25	147	5.0	243	1 US-08-726-160-6	Sequence 6, App11
26	147	5.0	243	5 PCT-US94-01782-6	Sequence 6, App11
27	146.5	5.0	688	4 US-08-973-273-26	Sequence 26, App11

28	146.5	5.0	747	4 US-08-973-273-3	Sequence 3, App11
29	145.5	4.9	414	1 US-07-667-276A-4	Sequence 4, App1
30	140.5	4.8	655	4 US-09-347-833-4	Sequence 4, App1
31	139	4.7	444	1 US-07-881-075-3	Sequence 3, App1
32	139	4.7	444	1 US-08-120-827-3	Sequence 3, App11
33	139	4.7	444	1 US-08-478-675-3	Sequence 3, App11
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35	133.5	4.5	359	1 US-08-120-827-2	Sequence 2, App11
36	133.5	4.5	359	1 US-08-478-675-2	Sequence 2, App11
37	133	4.5	380	1 US-07-881-075-51	Sequence 51, App1
38	133	4.5	380	1 US-08-120-827-51	Sequence 51, App1
39	133	4.5	380	1 US-08-478-675-51	Sequence 51, App1
40	132	4.5	443	2 US-08-935-450-6	Sequence 6, App1
41	129.5	4.4	545	2 US-08-990-114-1	Sequence 1, App1
42	129.5	4.4	545	4 US-09-241-333-1	Sequence 1, App1
43	129	4.4	675	4 US-08-973-273-5	Sequence 5, App11
44	127	4.3	652	4 US-09-347-833-2	Sequence 2, App11
45	122.5	4.1	428	4 US-09-347-833-6	Sequence 6, App11

#### ALIGNMENTS

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RESULT 1
US-09-643-597-176
; Sequence 176, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-176
100.0% Score 2956; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKLYIGNLSNNAAPSDLESIFPKDKIPYSGPPLVKTGYAFVDCDESMALKALEALSCK 60
DB 1 MNKLYIGNLSNNAAPSDLESIFPKDKIPYSGPPLVKTGYAFVDCDESMALKALEALSCK 60
QY 61 IELHCKPFEVSHVSPKQRIRKIQIRNIPPHLOWEVLDSLVOXGVNSCEQVNTDSETA 120
DB 61 IELHCKPFEVSHVSPKQRIRKIQIRNIPPHLOWEVLDSLVOXGVNSCEQVNTDSETA 120
QY 121 VVNVYSSKKDARALDKLNGFLENFTLKVAITPEMAAQQNPLOQPRGRGRGGGGSS 180
DB 121 VVNVYSSKKDARALDKLNGFLENFTLKVAITPEMAAQQNPLOQPRGRGRGGGGSS 180
QY 181 ROGSGVSVKQPCDPLRLVLPFOEVGAILGEGATIRNTKOTOSKIDVHRKENGAA 240
DB 181 ROGSGVSVKQPCDPLRLVLPFOEVGAILGEGATIRNTKOTOSKIDVHRKENGAA 240
QY 241 EKSTIIILSTPGTSAACKSILIEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300
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Db 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEEIPKTLAHNNFVGRILGEGRNK 300
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Db 301 KIEODTDTKITITSPLOELTYNPERTITVKGWETCAKAEEMKIKIESENDIASMNL 360
Oy 361 QAHILPGILNLTALGLFPTSGMPPTSGPPSAMTPPYPOFOSSTETVHOFIPALSVGAI 420
Db 361 QAHILPGILNLTALGLFPTSGMPPTSGPPSAMTPPYPOFOSSTETVHOFIPALSVGAI 420
Oy 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRVVIITGPPEAOFKAOGRIYKIKEENFV 480
Db 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRVVIITGPPEAOFKAOGRIYKIKEENFV 480
Oy 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELOJLSSAEVVPDPOTPDENDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELOJLSSAEVVPDPOTPDENDQVVKIT 540
Oy 541 GHFYACQVQAKRKIOEILITVOKHOQOKALQSGPPSRRK 579
Db 541 GHFYACQVQAKRKIOEILITVOKHOQOKALQSGPPSRRK 579

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## RESULT 2

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US-09-643-597-348
? Sequence 348, Application US/09643597
? Patent No. 6426072
? GENERAL INFORMATION:
? APPLICANT: Wang, Tonglong
? APPLICANT: Fan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aljun
? APPLICANT: Skelky, Yasir A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.453C11
? CURRENT APPLICATION NUMBER: US/09/643,597
? CURRENT FILING DATE: 2000-08-21
? NUMBER OF SEQ ID NOS: 369
? SOFTWARE: SeqEd for Windows Version 3.0
? SEQ ID NO 348
? LENGTH: 579
? TYPE: prt
? ORGANISM: Homo sapiens
US-09-643-597-348

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Query Match 99.6%; Score 2943; DB 4; Length 579;
Best Local Similarity 99.7%; Pred. No. 2,4e-25;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 IELHGPRIEHSVYKROKRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
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Db 181 ROGSPGYSKQKRCDDPLRLVLPYOPFGAIIIGKGAATINITKQOSKIDYHKKENAGA 240

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Oy 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEEIPKTLAHNNFVGRILGEGRNK 300
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Db 361 QAHILPGILNLTALGLFPTSGMPPTSGPPSAMTPPYPOFOSSTETVHOFIPALSVGAI 420
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Db 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRVVIITGPPEAOFKAOGRIYKIKEENFV 480
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Db 541 GHFYACQVQAKRKIOEILITVOKHOQOKALQSGPPSRRK 579

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## RESULT 3

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US-09-261-855-2
? Sequence 2, Application US/09261855A
? Patent No. 6255055
? GENERAL INFORMATION:
? APPLICANT: Ross, Jeffrey
? TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
? TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
? FILE REFERENCE: 960296.95131
? CURRENT APPLICATION NUMBER: US/09/261,855A
? CURRENT FILING DATE: 1999-03-03
? NUMBER OF SEQ ID NOS: 46
? SOFTWARE: Patentia Ver. 2.0
? SEQ ID NO 2
? LENGTH: 577
? TYPE: prt
? ORGANISM: Mus musculus
US-09-261-855-2

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Query Match 74.18%; Score 2190; DB 4; Length 577;
Best Local Similarity 74.18%; Pred. No. 4.3e-187;
Matches 434; Conservative 62; Mismatches 74; Indels 16; Gaps 8;

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Oy 1 MNKLYIGNLSNAPSDLSIFKDAKIPVSGPFLVKTGYAFVDCPDSEMAKALAEALSG 60
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Db 61 IELHGPRIEHSVYKROKRIKQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
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Db 237 AGAENSITLSTPECTSAACKSILEIMHKEADIKFTEEIPKTLAHNNFVGRILGEG 296
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Db 297 RNKAKYEDTETKITISSLDQDLTINPERTITVKGWETCAKAEEMKIKIESENDIA 356
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Db 414 AQAAGATIGKGGHIOKLSFASASIKTAPETPSKVRWYITGPEAFKQKGTIK 473
Qy 474 IKENFVSPKEEVKLEAHIRVPSFAGRYIGKGTYNELQNLSSAEVVPDQTPDEND 533
Db 474 LKENFPGPEEVKLEHIRVPSASAGRYIGKGTYNELQNLSSAEVVPDQTPDEND 533
Qy 534 QVVVKITGFYACQVAAKRIQELITQVQKQKALQSGPQSRK 579
Db 534 QVVKITGFYASQMAQRKIRDLAQVKQ-QHQKQ-QSNLAQARR 577

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## RESULT 4

```

US-08-021-608D-2
Sequence 2, Application US/08021608D
Patent No. 5580760

```

```

GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHEICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HD60
FEATURE:
OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile
US-08-021-608D-2

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Query Match 8.2%; Score 241; DB 1; Length 644;
Best Local Similarity 22.3%; Pred. No. 5,66-13;
Matches 100; Conservative 75; Mismatches 154; Indels 120; Gaps 17;

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Qy 161 QONPLQ---OPRGRGLGGRSGSGSGSVSKQPCOLPLRLLYPQFVAGALIGKEGAT 217
Db 63 QKRFLEDDOPDPDAKVAPOWDSFTGLPRMHQOQSRSVTEETVYVPGMWGFTLIGGGEQ 122
Qy 218 IRNTKQTSKIDVHKRENAGAESTITLSTPEGSTACKSILEIMKKAQDIKTE--- 275
Db 123 ISRIQESGCKIQI-APDSGGLPERSCXLTGPEVSQAKKLDQIYEKRAPAGNHCD 181.
Qy 276 ---ELPILILANNNFVGRLLGKEGRNLKKIEDDTTKITLISPLQELTYNPERT----- 327
Db 182 GPGNAVOEIMIPASKAGLVIGKGETIKQLQERAAQKVMW---IQD-----GPQNTGADKPL 235
Qy 328 TVKGVNTECAKAEIEIKKIRE-----SYENDIASMNLQAILIGLNLGLFPPSGM 382
Db 236 RITGDPYVQAKEMVELIRDQGGFREVRNKGSR-----IG-----NKG1 278
Qy 383 PPPTSGPPSAMTPPYQFQESFETVHOFIPALSVGATIGKOGHIOKLSFAPASIKTA 442
Db 279 DVP-----IPRFVGIYIGRNGEMIKKIQNDAGVRIQK 312
Qy 443 PAEPDAKVRWYITGPE-AQPKAO-----GRITK----- 473
Db 313 PDDGTPPE-RIAQITGPPRCQHAAEITDILRSVQAGNPGSGGGRGQGMNMG 371
Qy 474 ---IKENFVSPKEEVKLEAHIRVPSFAGRYIGKGTYNELQNLSSAEVVPDQTP 529
Db 372 PPGGLQEFNFI-----VPTGKTGLITGKGETIKSISQSGARIELQKPP 418
Qy 530 DENDOV-VVKITGFH---FYACQVAAQRK 553
Db 419 MADPMKLFITRGTPOQIDVARLIIEKI 447

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## RESULT 5

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US-07-726-160-2
Sequence 2, Application US/07726160
Patent No. 5734016

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GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644

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Db 419 NAOPNMKLETTIGTPOQIDYAROLIEKI 447

## RESULT 7

US-09-261-855-22  
Sequence 22, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: ROSS, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261.855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 49  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-261-855-22

## Query Match

Best Local Similarity 98.0%; Score 238; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2e-14;  
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## YQ 281

ILAHNNFVGRLLGKGRMLKKIEODTDTKTIISPLQELTLYNPRTIYV 329  
1 ILAHNNFVGRLLGKGRMLKKIEODTDTKTIISPLQELTLYNPRTIYV 49

## RESULT 8

US-09-261-855-24  
Sequence 24, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: ROSS, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261.855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-261-855-24

## Query Match

Best Local Similarity 100.0%; Score 237; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.3e-14;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## YQ 492

IRVPSFAGRVIGKGGKTYNELONLSAEVVPDPDPPNDVVYKI 539  
1 IRVPSFAGRVIGKGGKTYNELONLSAEVVPDPDPPNDVVYKI 48

## RESULT 9

US-08-021-608D-10  
Sequence 10, Application US/08021608D  
Patent No. 5580760  
GENERAL INFORMATION:  
APPLICANT: LEVENS, DAVID L., DUNCAN,  
APPLICANT: ROBERT C., AND AVTGAN, MARK I.  
TITLE OF INVENTION: NOVEL FUSE BINDING  
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESS: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK

STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/021.608D  
FILING DATE: 22-FEB-1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: WILLIAM S. FELLER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4063

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 643

TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide/Protein  
HYPOTHETICAL: No  
ORIGINAL SOURCE:

ORGANISM: Human  
CELL LINE: HL60

FEATURE:  
OTHER INFORMATION:

OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile

US-08-021-608D-10

Query Match

Best Local Similarity 8.0%; Score 236.5; DB 1; Length 643;  
Best Local Similarity 22.3%; Pred. No. 1.4e-12;  
Matches 100; Conservative 77; Mismatches 151; Indels 121; Gaps 16;

YQ 161 GONPLQ---OPRRGRGIGSGSSRSGSPGSVSKRCDLPLRLVLPYQFATIGKGGAT 217  
Db 63 OKRPLEDGDOPDAKVAAPQNDSTFGTLP-PMHQOQSVYTEKRYVPGMGVFTIGRGGED 121

YQ 218 IRNITKOTOSKIDVHKRENGAAEKSTITLSTPEGSTAACKSILEMKREADIKETE-- 275  
Db 122 ISRIDGESCKIQI-APDSGLPERSCXLTGTPESVQSAKRLLDQIVKGRPAFGFHGD 180

YQ 276 ---ETPLKILAHNNFVGRLLGKGRMLKKIEODTDTKTIISPLQELTLYNPRTIYV 327  
Db 181 GPGNAVQEIPIPAKAGLIVGKGGKTYNELONLSAEVVPDPDPPNDVVYKI 234

YQ 328 TYKGNVETCAKAEELMKKTRF-----SYENDIASMNLOAHLIGLNMNLGLEPPPSGM 382  
Db 235 RITGDPYKVOQAKMVALELIRDDGGFREVRYNEGSR-----IGS-----NEGI 277

YQ 383 PPTSGPPSAMPYPPQFQSETEYVHOPILALISGAILIGKGGKTYNELONLSAEVVPDPDPPNDVVYKI 442  
Db 278 DVP-----IPRFAGIVYGRNGEIKKIDNADGVRIOFK 311

YQ 443 PAEAPDAKRVAVITGPPE-AQFKAQ-----GRIVK----- 473  
Db 312 PDDGTTP-RLAQITGTPDRGQHAALITDLRSVQAGNPGGPGGGRGRGGMNMG 370

YQ 474 ---IKENFVSKPEVEKLEAHIRVPSFAGRVIGKGGKTYNELONLSAEVVPDPDPPNDVVYKI 529  
Db 371 PPGGLQEPNFI-----VPTGKGLIGKGGKTYNELONLSAEVVPDPDPPNDVVYKI 417

YQ 530 DENDOV-VVKITGH---FYACVQAQRKI 553  
Db 530 DENDOV-VVKITGH---FYACVQAQRKI 553





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Page 8

Db 281 MIKIONDAGVRIQFKPDGTTPE-RIAQITGPPRCQAHAEITDILRSVOAGNPGGPG 339  
Qy 468 --GRIYK-----IKENFVSKREVKLEAHIRVSPFAGRVIGCKGTVEL 513  
Db 340 PGRGRGROGGMNMPPGGLQEFNFI-----VPTGKTGLIGGGETIKSI 386  
Qy 514 QNLSAEVVPPDQTPDENOV-VVKITGH---FYACQVAKRKI 553  
Db 387 SQSGARIELOHNPNNADPNMKLFTIRGTPQIDYARQLIEEKI 431

RESULT 14  
US-08-726-160-8  
Sequence 8, Application US/08726160  
Patent No. 5714016

GENERAL INFORMATION:  
APPLICANT: LEVENS, DAVID L., DUNCAN,  
APPLICANT: ROBERT C., AND AVIGAN, MARK I.  
TITLE OF INVENTION: NOVEL FUSE BINDING  
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,160  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/021,608  
FILING DATE: 22-FEB-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4063US1  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 590  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide/Protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
CELL LINE: HL60  
US-08-726-160-8

US-08-726-160-8

Query Match 7.88; Score 229.5; DB 1; Length 590;  
Best Local Similarity 22.5%; Pctd. No. 5.2e-12;  
Matches 91; Conservative 69; Mismatches 128; Indels 117; Gaps 16;

Qy 202 VPTQVGAITGEGATIRNITKOTSKIDVHRKENAGAKESITLITSTEGTSAACKSIL 261  
Db 91 VPDQWVGLTIGRGEQISRLQOESGCKIOT-APDSGGGLPERSCMLTGTPESVQSKRLLD 149  
Qy 262 EIMAKRADIKTE-----ELPIKIIAHNNFVGRILGEGRNLIKITEQDTDTKTIISFLQ 316  
Db 150 QIVKGRPAFGFHDGDFGNANVQDIMPASKAGLVISGGGTIKQLQERAGYKVMV--IQ 207

Qy 317 ELTVNPERT-----ITYKGNVETCAKAEELIMKIRE-----STENDIASNNLOAHILP 366  
Db 208 D---GQNTGADKPLRTITGDPKVOAKENVLEIRQGGFREVNRGSR-----IG 257  
Qy 367 GLNMLGLFPPTSGMPPTSGPSANTPTYPQFQSTETVHOFIIPALSNALIGKQO 426  
Db 258 G-----NEGIDVP-----IPRAVGIAGRNGE 280  
Qy 427 HIKQLSPGASIKTAFAEADAKVPMVITGPRE-NGFNQ----- 467  
Db 281 MIKIONDAGVRIQFKPDGTTPE-RIAQITGPPRCQAHAEITDILRSVOAGNPGGPG 339  
Qy 468 --GRIYK-----IKENFVSKREVKLEAHIRVSPFAGRVIGCKGTVEL 513  
Db 340 PGRGRGROGGMNMPPGGLQEFNFI-----VPTGKTGLIGGGETIKSI 386  
Qy 514 QNLSAEVVPPDQTPDENOV-VVKITGH---FYACQVAKRKI 553  
Db 387 SQSGARIELOHNPNNADPNMKLFTIRGTPQIDYARQLIEEKI 431

RESULT 15  
PCT-US94-01782-8  
Sequence 8, Application PC/TUS9401782  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES  
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF  
HEALTH AND HUMAN SERVICES  
TITLE OF INVENTION: NOVEL FUSE BINDING  
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01782  
FILING DATE: 22-FEB-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/021,608  
FILING DATE: 22-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4063PCT  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 590  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide/Protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
CELL LINE: HL60  
US-08-726-160-8

Qy 202 VPTQVGAITGEGATIRNITKOTSKIDVHRKENAGAKESITLITSTEGTSAACKSIL 261  
Db 91 VPDQWVGLTIGRGEQISRLQOESGCKIOT-APDSGGGLPERSCMLTGTPESVQSKRLLD 149  
Qy 262 EIMAKRADIKTE-----ELPIKIIAHNNFVGRILGEGRNLIKITEQDTDTKTIISFLQ 316  
Db 150 QIVKGRPAFGFHDGDFGNANVQDIMPASKAGLVISGGGTIKQLQERAGYKVMV--IQ 207

CELL LINE: HL60  
ORGANELLE:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PCT-US94-01782-8

Query Match 7.88; Score 229.5; DB 5; Length 590;  
Best Local Similarity 22.58; Pred. No. 5.2e-12;  
Matches 91; Conservative 69; Mismatches 128; Indels 117; Gaps 16;

QY 202 VPTQFYGATIGEGATINIKKQOSKIDVHRKEMAGAEKSTILSTPGTSACKSIL 261  
DB 91 VPDGAVGFTIGRGEOISRIQOESCKIQT-APDSGGLPERSCMLTGTPEVSQAKRLD 149  
QY 262 EIMHKEADIKFTE---EIPKLIANNFVGRILIGKEGKLNKKIIBQDTTKITISPLQ 316  
DB 150 QIVEKGRPAFGFHGDGPGNAVOEIMIPASKAGLVIKGGFTIKOLOERAGVKKVM--IQ 207  
QY 317 ELTYMPERT---ITVGNVETCAKAEEDIMKIRE---SYENDIASMNLQAHLP 366  
DB 208 D---GPGNTGADKPLRTIGDPYKQAKEMVLELIRDGGFREVNRNYSR-----IG 257  
QY 367 GLNLNALGLPPTSGMPPTSGPPSAMTPPYPOFQOSEFTVHOFTIPALSVGAILIGKQO 426  
DB 258 G-----NEGIDVP-----IPRFVGIIVIGRNGE 280  
QY 427 HIKOLSRFAGASIKIAPAEAPDAKVMYITGPE-AQFKAO----- 467  
DB 281 MIKKIONDAGVRIQFKRPDGTPE-RIAQITGPPDRCHMAEITDILRSVQAGNPGPG 339  
QY 468 --GRITGK-----IKENFVSPKEEVKLEAHIRVPSFAGRVIGKGGKTYNEL 513  
DB 340 PGGRRGRGOGMMNMNGPPGGLQEFNFI-----VPTGKTGLIIGKGGETIKSI 386  
QY 514 QNLSSAEVVVPRDQTPENDQV-VYKITGH---FYACQVAORKI 553  
DB 387 SQOOGARIELORNPNDPNMKLFTIRGTPOQIDYARQLIEKI 431

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Job time : 36.3251 secs



Thu Apr 17 07:55:18 2003

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Page 1

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:19:20 ; Search time 388.852 Seconds  
(without alignments)  
960.006 Million cell updates/sec

Title: US-09-897-778-176  
Perfect score: 2956  
Sequence: 1 MNKLYIGLSENAFSDLES.....VKHQDQKALQSGPPQSRRK 579

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents-AA>Main:\*  
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4: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
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25: /cgn2\_6/ptodata/1/paa/US063\_COMB.pep:\*  
26: /cgn2\_6/ptodata/1/paa/US062\_COMB.pep:\*  
27: /cgn2\_6/ptodata/1/paa/US061\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	2956	100.0	579	1	PCT-US01-47576-176
2	2956	100.0	579	18	US-09-466-396A-176
3	2956	100.0	579	18	US-09-476-196A-176
4	2956	100.0	579	18	US-09-480-884A-176
5	2956	100.0	579	19	US-09-510-376A-176
6	2956	100.0	579	19	US-09-542-615A-176

7	2956	100.0	579	20	US-09-606-421A-176	Sequence 176, App
8	2956	100.0	579	20	US-09-606-421B-176	Sequence 176, App
9	2956	100.0	579	20	US-09-630-940A-176	Sequence 176, App
10	2956	100.0	579	20	US-09-630-940B-176	Sequence 176, App
11	2956	100.0	579	20	US-09-662-786-176	Sequence 176, App
12	2956	100.0	579	20	US-09-685-696-176	Sequence 176, App
13	2956	100.0	579	21	US-09-735-705-176	Sequence 176, App
14	2956	100.0	579	21	US-09-791-537-49019	Sequence 49019, A
15	2956	100.0	579	22	US-09-850-716A-176	Sequence 176, App
16	2956	100.0	579	22	US-09-897-778-176	Sequence 176, App
17	2956	100.0	579	22	US-10-007-700-176	Sequence 176, App
18	2956	100.0	579	24	US-10-117-982-176	Sequence 176, App
19	2956	100.0	579	21	PCT-US01-47576-348	Sequence 348, App
20	2949	99.8	579	21	PCT-US01-47576-446	Sequence 446, App
21	2943	99.6	579	1	PCT-US01-47576-449	Sequence 449, App
22	2943	99.6	579	19	US-09-542-615A-348	Sequence 348, App
23	2943	99.6	579	20	US-09-606-421A-348	Sequence 348, App
24	2943	99.6	579	20	US-09-606-421B-348	Sequence 348, App
25	2943	99.6	579	20	US-09-630-940A-348	Sequence 348, App
26	2943	99.6	579	20	US-09-662-786-348	Sequence 348, App
27	2943	99.6	579	20	US-09-685-696-348	Sequence 348, App
28	2943	99.6	579	20	US-09-735-705-348	Sequence 348, App
29	2943	99.6	579	22	US-09-850-716A-348	Sequence 348, App
30	2943	99.6	579	22	US-09-897-778-446	Sequence 446, App
31	2943	99.6	579	22	US-10-007-700-446	Sequence 446, App
32	2943	99.6	579	24	US-10-117-982-446	Sequence 446, App
33	2943	99.6	579	25	US-10-117-982-449	Sequence 449, App
34	2943	99.6	579	25	US-10-117-982-449	Sequence 449, App
35	2943	99.6	579	25	US-10-117-982-480	Sequence 480, App
36	2943	99.6	579	25	PCT-US01-47576-427	Sequence 427, App
37	2943	99.6	579	22	US-09-850-716-427	Sequence 427, App
38	2943	99.6	579	24	US-10-007-700-446	Sequence 446, App
39	2943	99.6	579	24	US-10-007-700-449	Sequence 449, App
40	2943	99.6	579	25	US-10-117-982-348	Sequence 348, App
41	2943	99.6	579	25	US-10-117-982-446	Sequence 446, App
42	2943	99.6	579	25	US-10-117-982-449	Sequence 449, App
43	2943	99.6	579	25	US-10-117-982-480	Sequence 480, App
44	2938	99.4	586	1	PCT-US01-47576-427	Sequence 427, App
45	2938	99.4	586	22	US-09-850-716-427	Sequence 427, App

#### ALIGNMENTS

RESULT 1  
PCT-US01-47576-176  
Sequence 176 Application PC/TUS0147576  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tonglong  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margareta  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Peckman, David W.  
APPLICANT: Cal, Feng  
APPLICANT: Foy, Teresa M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.45503PC  
CURRENT APPLICATION NUMBER: PCT/US01/47576  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FastSeq for Windows Version 4.0

Thu Apr 17 07:55:18 2003

us-09-897-778-176.ram

Page 2

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; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-176

Query Match
Best Local Similarity 100.0%; Score 2956; DB 1; Length 579;
Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSCK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSCK 60
QY 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVYGVVESCQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVYGVVESCQVNTDSETA 120
QY 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAVYIPDEMAAQNPLQOPRGRGLGGRSS 180
DB 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAVYIPDEMAAQNPLQOPRGRGLGGRSS 180
QY 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKGEATIRNITKOTQSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKGEATIRNITKOTQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFVGRIGKEGRNLK 300
DB 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFVGRIGKEGRNLK 300
QY 301 KIEODDTKITISPLQELTLYNPERTTYKGNVETCAKAEEMKIRESEYENDIASMNL 360
DB 301 KIEODDTKITISPLQELTLYNPERTTYKGNVETCAKAEEMKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNMLNLGFPPTSGMPPTSGPSPAMTPPYQFQSETEYVHOFPALSVGAI 420
DB 361 QAHLIPGLNMLNLGFPPTSGMPPTSGPSPAMTPPYQFQSETEYVHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMVYITGPPEAOKRAGRYGKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMVYITGPPEAOKRAGRYGKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVYVPRDQTPDENOVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVYVPRDQTPDENOVVVKIT 540
QY 541 GHFYACOVAQRKIOEILTVOKHOQKALOSGPPQSRK 579
DB 541 GHFYACOVAQRKIOEILTVOKHOQKALOSGPPQSRK 579

RESULT 2
US-09-466-396A-176
; Sequence 176, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466, 396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-396A-176

Query Match
Best Local Similarity 100.0%; Score 2956; DB 18; Length 579;
Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSCK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSCK 60
QY 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVYGVVESCQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVYGVVESCQVNTDSETA 120
QY 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAVYIPDEMAAQNPLQOPRGRGLGGRSS 180
DB 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAVYIPDEMAAQNPLQOPRGRGLGGRSS 180
QY 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKGEATIRNITKOTQSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKGEATIRNITKOTQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFVGRIGKEGRNLK 300
DB 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFVGRIGKEGRNLK 300
QY 301 KIEODDTKITISPLQELTLYNPERTTYKGNVETCAKAEEMKIRESEYENDIASMNL 360
DB 301 KIEODDTKITISPLQELTLYNPERTTYKGNVETCAKAEEMKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNMLNLGFPPTSGMPPTSGPSPAMTPPYQFQSETEYVHOFPALSVGAI 420
DB 361 QAHLIPGLNMLNLGFPPTSGMPPTSGPSPAMTPPYQFQSETEYVHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMVYITGPPEAOKRAGRYGKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMVYITGPPEAOKRAGRYGKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVYVPRDQTPDENOVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVYVPRDQTPDENOVVVKIT 540
QY 541 GHFYACOVAQRKIOEILTVOKHOQKALOSGPPQSRK 579
DB 541 GHFYACOVAQRKIOEILTVOKHOQKALOSGPPQSRK 579

RESULT 3
US-09-476-496A-176
; Sequence 176, Application US/09476496A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Katos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476, 496A
; CURRENT FILING DATE: 1999-12-30.
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-496A-176

Query Match
Best Local Similarity 100.0%; Score 2956; DB 18; Length 579;
Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSCK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSCK 60
QY 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVYGVVESCQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVYGVVESCQVNTDSETA 120
QY 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAVYIPDEMAAQNPLQOPRGRGLGGRSS 180
DB 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAVYIPDEMAAQNPLQOPRGRGLGGRSS 180
QY 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKGEATIRNITKOTQSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKGEATIRNITKOTQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFVGRIGKEGRNLK 300
DB 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFVGRIGKEGRNLK 300
QY 301 KIEODDTKITISPLQELTLYNPERTTYKGNVETCAKAEEMKIRESEYENDIASMNL 360
DB 301 KIEODDTKITISPLQELTLYNPERTTYKGNVETCAKAEEMKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNMLNLGFPPTSGMPPTSGPSPAMTPPYQFQSETEYVHOFPALSVGAI 420
DB 361 QAHLIPGLNMLNLGFPPTSGMPPTSGPSPAMTPPYQFQSETEYVHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMVYITGPPEAOKRAGRYGKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVMVYITGPPEAOKRAGRYGKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVYVPRDQTPDENOVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVYVPRDQTPDENOVVVKIT 540
QY 541 GHFYACOVAQRKIOEILTVOKHOQKALOSGPPQSRK 579
DB 541 GHFYACOVAQRKIOEILTVOKHOQKALOSGPPQSRK 579
```



```

QY 121 VVNTYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
    |||
Db 121 VVNTYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
QY 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240
    |||
Db 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240
QY 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
    |||
Db 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
QY 301 KIEODDTKTITSPLOELTYNPERTITVKNVETCAAEIEIMKKITRESYENDIASMNL 360
    |||
Db 301 KIEODDTKTITSPLOELTYNPERTITVKNVETCAAEIEIMKKITRESYENDIASMNL 360
QY 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
    |||
Db 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAPKAGRIYGIKEENFY 480
    |||
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAPKAGRIYGIKEENFY 480
QY 481 SPKEEVLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVVPDQTPDENQVYVKIT 540
    |||
Db 481 SPKEEVLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVVPDQTPDENQVYVKIT 540
QY 541 GHFYACVQVQARKIOEILTYVKOHQOQKALQSGPPQSRK 579
    |||
Db 541 GHFYACVQVQARKIOEILTYVKOHQOQKALQSGPPQSRK 579

```

## RESULT 4.

```

US-09-480-884A-176
: Sequence 176, Application US/09480884A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45356
: CURRENT APPLICATION NUMBER: US/09/480, 884A
: CURRENT FILING DATE: 2001-08-27
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRN
: ORGANISM: Homo sapiens
US-09-480-884A-176

```

```

Query Match 100.0%; Score 2956; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
    |||
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
QY 61 IELHGKPIEVEHVSVPKROIRIKIQRINIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
    |||
Db 61 IELHGKPIEVEHVSVPKROIRIKIQRINIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
QY 121 VVNTYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
    |||
Db 121 VVNTYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
QY 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240
    |||
Db 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240

```

```

Db 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240
    |||
QY 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
    |||
Db 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
QY 301 KIEODDTKTITSPLOELTYNPERTITVKNVETCAAEIEIMKKITRESYENDIASMNL 360
    |||
Db 301 KIEODDTKTITSPLOELTYNPERTITVKNVETCAAEIEIMKKITRESYENDIASMNL 360
QY 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
    |||
Db 361 QAHLIPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAPKAGRIYGIKEENFY 480
    |||
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAPKAGRIYGIKEENFY 480
QY 481 SPKEEVLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVVPDQTPDENQVYVKIT 540
    |||
Db 481 SPKEEVLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVVPDQTPDENQVYVKIT 540
QY 541 GHFYACVQVQARKIOEILTYVKOHQOQKALQSGPPQSRK 579
    |||
Db 541 GHFYACVQVQARKIOEILTYVKOHQOQKALQSGPPQSRK 579

```

## RESULT 5

```

US-09-510-376A-176
: Sequence 176, Application US/09510376A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45557
: CURRENT APPLICATION NUMBER: US/09/510, 376A
: CURRENT FILING DATE: 2001-08-21
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRN
: ORGANISM: Homo sapiens
US-09-510-376A-176

```

```

Query Match 100.0%; Score 2956; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
    |||
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
QY 61 IELHGKPIEVEHVSVPKROIRIKIQRINIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
    |||
Db 61 IELHGKPIEVEHVSVPKROIRIKIQRINIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
QY 121 VVNTYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
    |||
Db 121 VVNTYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
QY 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240
    |||
Db 181 ROSPGSVSKOKPCDPLRLILVPTQFVGAIIKGEKATIRNITKOTOSKIDVHRKENGAA 240
QY 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
    |||
Db 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300

```

```
OY 301 KIEODDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRRESYENDIASNL 360
DB 301 KIEODDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRRESYENDIASNL 360
OY 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
DB 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSAEVVPRDQTPDENDDQVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSAEVVPRDQTPDENDDQVVKIT 540
OY 541 GHFYACQVAKRKIOEILITOVKHOQOKALOSGPQSRK 579
DB 541 GHFYACQVAKRKIOEILITOVKHOQOKALOSGPQSRK 579

RESULT 6
US-09-542-615A-176
; Sequence 176, Application US/09542615A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Katos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skeiky, Yasser A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-176

Query Match 100.0%; Score 2956; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
OY 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 120
OY 121 VVAVTSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRLGGRGSS 180
DB 121 VVAVTSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRLGGRGSS 180
OY 181 RQSPGSVSKQPCDPLRLVLPQFVGAILGEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKQPCDPLRLVLPQFVGAILGEGATIRNITKQTSKIDVHRKENAGAA 240
OY 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEEIPKLILAHNNEVGRILGEGRNK 300
DB 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEEIPKLILAHNNEVGRILGEGRNK 300
OY 301 KIEODDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRRESYENDIASNL 360
DB 301 KIEODDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRRESYENDIASNL 360
OY 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
DB 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
```

```
OY 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
DB 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSAEVVPRDQTPDENDDQVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSAEVVPRDQTPDENDDQVVKIT 540
OY 541 GHFYACQVAKRKIOEILITOVKHOQOKALOSGPQSRK 579
DB 541 GHFYACQVAKRKIOEILITOVKHOQOKALOSGPQSRK 579

RESULT 7
US-09-606-421A-176
; Sequence 176, Application US/09606421A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Katos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skeiky, Yasser A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/606.421A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421A-176

Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
OY 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVOYGVESECEQVNTDSETA 120
OY 121 VVAVTSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRLGGRGSS 180
DB 121 VVAVTSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQNPLQOPRGRRLGGRGSS 180
OY 181 RQSPGSVSKQPCDPLRLVLPQFVGAILGEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKQPCDPLRLVLPQFVGAILGEGATIRNITKQTSKIDVHRKENAGAA 240
OY 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEEIPKLILAHNNEVGRILGEGRNK 300
DB 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEEIPKLILAHNNEVGRILGEGRNK 300
OY 301 KIEODDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRRESYENDIASNL 360
DB 301 KIEODDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRRESYENDIASNL 360
OY 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
DB 361 QAHILPGNLNMGALGFPPTSGMPPTSGPSAMTPPYPOFQOSEETVHOIFALSVGI 420
```

Db 361 QAHILPGLNLTALGLFPPTSGMPPTSGPPSANTPPYPQFQESQETETTHQFIPLASVGA1 420  
Qy 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRITGKIKEENFV 480  
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRITGKIKEENFV 480  
Qy 481 SPKEEVYLEHIVSPFAAGRVIGKGGKTVNELONLSSAEVVPDQTPDENDDVYVYKIT 540  
Db 481 SPKEEVYLEHIVSPFAAGRVIGKGGKTVNELONLSSAEVVPDQTPDENDDVYVYKIT 540  
Qy 541 GHFYACQVAORRKOIEILLTVYKHOQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORRKOIEILLTVYKHOQOKALQSGPPQSRK 579

## RESULT 8

US-09-606-421B-176  
; Sequence 176, Application US/09606421B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606,421B  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-606-421B-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 8,6e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSCK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSCK 60  
Qy 61 TELHGRLEVEHSPKQRIRKQIRINIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
Db 61 TELHGRLEVEHSPKQRIRKQIRINIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
Qy 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQONPLQOPRGRGLGQSGSS 180  
Db 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQONPLQOPRGRGLGQSGSS 180  
Qy 181 ROGSPGSVSKQKQDPLRLVLVPTQFVGAIIGEGATINNTKQOSKIDVHKKENAGAA 240  
Db 181 ROGSPGSVSKQKQDPLRLVLVPTQFVGAIIGEGATINNTKQOSKIDVHKKENAGAA 240  
Qy 241 EKSTIILSTPEGTSAAKSLIEMHKEADIKFTEERIPKLILAHNNFVGRILGKGRNLK 300  
Db 241 EKSTIILSTPEGTSAAKSLIEMHKEADIKFTEERIPKLILAHNNFVGRILGKGRNLK 300  
Qy 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETCAKAEELIMKKIRSYENDIASMNL 360  
Db 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETCAKAEELIMKKIRSYENDIASMNL 360  
Qy 361 QAHILPGLNLTALGLFPPTSGMPPTSGPPSANTPPYPQFQESQETETTHQFIPLASVGA1 420  
Db 361 QAHILPGLNLTALGLFPPTSGMPPTSGPPSANTPPYPQFQESQETETTHQFIPLASVGA1 420

Qy 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRITGKIKEENFV 480  
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRITGKIKEENFV 480  
Qy 481 SPKEEVYLEHIVSPFAAGRVIGKGGKTVNELONLSSAEVVPDQTPDENDDVYVYKIT 540  
Db 481 SPKEEVYLEHIVSPFAAGRVIGKGGKTVNELONLSSAEVVPDQTPDENDDVYVYKIT 540  
Qy 541 GHFYACQVAORRKOIEILLTVYKHOQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORRKOIEILLTVYKHOQOKALQSGPPQSRK 579

## RESULT 9

US-09-630-940A-176  
; Sequence 176, Application US/09630940A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C10  
; CURRENT APPLICATION NUMBER: US/09/630,940A  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-630-940A-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 8,6e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSCK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSCK 60  
Qy 61 TELHGRLEVEHSPKQRIRKQIRINIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
Db 61 TELHGRLEVEHSPKQRIRKQIRINIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
Qy 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQONPLQOPRGRGLGQSGSS 180  
Db 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQONPLQOPRGRGLGQSGSS 180  
Qy 181 ROGSPGSVSKQKQDPLRLVLVPTQFVGAIIGEGATINNTKQOSKIDVHKKENAGAA 240  
Db 181 ROGSPGSVSKQKQDPLRLVLVPTQFVGAIIGEGATINNTKQOSKIDVHKKENAGAA 240  
Qy 241 EKSTIILSTPEGTSAAKSLIEMHKEADIKFTEERIPKLILAHNNFVGRILGKGRNLK 300  
Db 241 EKSTIILSTPEGTSAAKSLIEMHKEADIKFTEERIPKLILAHNNFVGRILGKGRNLK 300  
Qy 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETCAKAEELIMKKIRSYENDIASMNL 360  
Db 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETCAKAEELIMKKIRSYENDIASMNL 360  
Qy 361 QAHILPGLNLTALGLFPPTSGMPPTSGPPSANTPPYPQFQESQETETTHQFIPLASVGA1 420  
Db 361 QAHILPGLNLTALGLFPPTSGMPPTSGPPSANTPPYPQFQESQETETTHQFIPLASVGA1 420

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Qy	421	IKGQOMHKKOLSRPAASAKITIPAEADPAVAVITITGPAAQKAGRIYKITEENFV	480
Db	421	IKGQOMHKKOLSRPAASAKITIPAEADPAVAVITITGPAAQKAGRIYKITEENFV	480
Qy	422	IKGQOMHKKOLSRPAASAKITIPAEADPAVAVITITGPAAQKAGRIYKITEENFV	480
Db	422	IKGQOMHKKOLSRPAASAKITIPAEADPAVAVITITGPAAQKAGRIYKITEENFV	480
Qy	481	SKPEEVKLEAHINVPFAAGRIYKIGKRTNELONSSAEVAVYRDOTPENDQVYVIT	540
Db	481	SKPEEVKLEAHINVPFAAGRIYKIGKRTNELONSSAEVAVYRDOTPENDQVYVIT	540
Qy	481	SKPEEVKLEAHINVPFAAGRIYKIGKRTNELONSSAEVAVYRDOTPENDQVYVIT	540
Db	481	SKPEEVKLEAHINVPFAAGRIYKIGKRTNELONSSAEVAVYRDOTPENDQVYVIT	540
Qy	541	GHFYACQVAAQRKIQELITLVYKQHQQAAALDSGPQSRKK	579
Db	541	GHFYACQVAAQRKIQELITLVYKQHQQAAALDSGPQSRKK	579
Qy	541	GHFYACQVAAQRKIQELITLVYKQHQQAAALDSGPQSRKK	579
Db	541	GHFYACQVAAQRKIQELITLVYKQHQQAAALDSGPQSRKK	579

```

RESULT 10
US-09-630-940B-176
Sequence 176, Application US/09630940B
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Ajun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45C10
CURRENT APPLICATION NUMBER: US/09/630.940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ. ID NOS: 367
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-630-940B-176

```

[illegible]

Qy	421	IKGQOHKLOLSFPAASAKIAPAEADAVRVVITITPEPAQKQKGIYKIKEENFV	480
	422	IKGQOHKLOLSFPAASAKIAPAEADAVRVVITITPEPAQKQKGIYKIKEENFV	480
Db	421	IKGQOHKLOLSFPAASAKIAPAEADAVRVVITITPEPAQKQKGIYKIKEENFV	480
Qy	481	SKPEEVLKLEHITVPEFAAGRTGKGYTNELONLSAEVYVPROPTDENDDQVYKIT	540
	482	SKPEEVLKLEHITVPEFAAGRTGKGYTNELONLSAEVYVPROPTDENDDQVYKIT	540
Db	481	SKPEEVLKLEHITVPEFAAGRTGKGYTNELONLSAEVYVPROPTDENDDQVYKIT	540
Qy	541	GHTFYACQVPAQRKIQELITLVYQHQQQALDGGPQSRKK	579
	542	GHTFYACQVPAQRKIQELITLVYQHQQQALDGGPQSRKK	579
Db	541	GHTFYACQVPAQRKIQELITLVYQHQQQALDGGPQSRKK	579

```

RESULT 11
US-09-662-786-176
Sequence 176, Application US/09662786
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yashir A W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121 45C12
CURRENT FILING DATE: 2000-09-15
CURRENT APPLICATION NUMBER: US/09/662,786
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-662-786-176

```

Query Match	100.0%	Score	2956;	DB	20;	Length	579;
Best Local Similarity	100.0%	Pred.	No. 8, 6e+24;				
Matches	579;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MNKLVTGNLSNAPSDLESIFKDAKIPVSGPFLVTKGVAFAVCCPDSEWALKATIEALSGK	60				
DB	1	MNKLVTGNLSNAPSDLESIFKDAKIPVSGPFLVTKGVAFAVCCPDSEWALKATIEALSGK	60				
QY	61	IELHCKPILEVSHSVPRKQRIRKIQIENIRPHLOMEVLDLSLVYGVESCEQVNDSEFA	120				
DB	61	IELHCKPILEVSHSVPRKQRIRKIQIENIRPHLOMEVLDLSLVYGVESCEQVNDSEFA	120				
QY	121	VYNAVYSSKDDARALDKLNGFLENFTLKVAATVPDEMAAOQNPLOQPRGRGCGGCGSS	180				
DB	121	VYNAVYSSKDDARALDKLNGFLENFTLKVAATVPDEMAAOQNPLOQPRGRGCGGCGSS	180				
QY	181	RGSGSGSVSKKPCDDPLRLVLTVPQVGAIIIGKSGATIRNITKOTQSKIDYHREKNGAA	240				
DB	181	RGSGSGSVSKKPCDDPLRLVLTVPQVGAIIIGKSGATIRNITKOTQSKIDYHREKNGAA	240				
QY	241	EXSITITSTPGSTGAACKSTILETMKKEODIKFPEELPLKILAHNNFVGRGLGEGGNLK	300				
DB	241	EXSITITSTPGSTGAACKSTILETMKKEODIKFPEELPLKILAHNNFVGRGLGEGGNLK	300				
QY	301	KLEQDTOPKRTITSPADQLTYNNEPRTYVKNQNTCAAEELTMKIRPSYENDIASNNL	360				
DB	301	KLEQDTOPKRTITSPADQLTYNNEPRTYVKNQNTCAAEELTMKIRPSYENDIASNNL	360				
QY	361	QAHILPGNLNALGLPPTSGPSPSAMPPTVQGEQSEETYNQTFPALSGAI	420				
DB	361	QAHILPGNLNALGLPPTSGPSPSAMPPTVQGEQSEETYNQTFPALSGAI	420				

QY 421 IKGOGHIKOLSRFAGASIKIAPAEADAKVNWIIITGPEAOFKAQGRIGKIKEENFV 480.  
|||||  
DB 421 IKGOGHIKOLSRFAGASIKIAPAEADAKVNWIIITGPEAOFKAQGRIGKIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAGAVIGKGTVNEIOLNLSAEEVVPDROTPENDQVYVKIT 540  
|||||  
DB 481 SPKEEVKLEAHIRVPSFAGAVIGKGTVNEIOLNLSAEEVVPDROTPENDQVYVKIT 540  
QY 541 GHFYACQVYAKRIQIEILLTVQVQHQQKALOSGPPQSRK 579  
|||||  
DB 541 GHFYACQVYAKRIQIEILLTVQVQHQQKALOSGPPQSRK 579

RESULT 12  
US-09-685-696-176  
; Sequence 176, Application US/09685696  
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaltanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C13  
; CURRENT APPLICATION NUMBER: US/09/685,696  
; CURRENT FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-685-696-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 8.6e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSGK 60  
|||||  
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSGK 60  
QY 61 IELHGKPIEVESHVPRKRIKLOIRNIPHLQWEVLDLSLVQGVVSECEQVNTDSETA 120  
|||||  
DB 61 IELHGKPIEVESHVPRKRIKLOIRNIPHLQWEVLDLSLVQGVVSECEQVNTDSETA 120  
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRLGGRSS 180  
|||||  
DB 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRLGGRSS 180  
QY 161 ROGSGSVSKORPCDPLRLVPTQFVGAILGKAGATIRNITKOTOSKIDVHKKENAGAA 240  
|||||  
DB 161 ROGSGSVSKORPCDPLRLVPTQFVGAILGKAGATIRNITKOTOSKIDVHKKENAGAA 240  
QY 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEELPLKILAHNNVGLIKKEGRNLK 300  
|||||  
DB 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEELPLKILAHNNVGLIKKEGRNLK 300  
QY 301 KIEODTDRKTIISPLQELTLYNPERTITVKGAVETCAKAEELMKKIRESEYENDIASMNL 360  
|||||  
DB 301 KIEODTDRKTIISPLQELTLYNPERTITVKGAVETCAKAEELMKKIRESEYENDIASMNL 360  
QY 361 QAHILPGILNALGLFPTSGMPPTSGPPSAMPPIPOEEOSETETVHOFIPALSVGAI 420  
|||||  
DB 361 QAHILPGILNALGLFPTSGMPPTSGPPSAMPPIPOEEOSETETVHOFIPALSVGAI 420

QY 421 IKGOGHIKOLSRFAGASIKIAPAEADAKVNWIIITGPEAOFKAQGRIGKIKEENFV 480  
|||||  
DB 421 IKGOGHIKOLSRFAGASIKIAPAEADAKVNWIIITGPEAOFKAQGRIGKIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAGAVIGKGTVNEIOLNLSAEEVVPDROTPENDQVYVKIT 540  
|||||  
DB 481 SPKEEVKLEAHIRVPSFAGAVIGKGTVNEIOLNLSAEEVVPDROTPENDQVYVKIT 540  
QY 541 GHFYACQVYAKRIQIEILLTVQVQHQQKALOSGPPQSRK 579  
|||||  
DB 541 GHFYACQVYAKRIQIEILLTVQVQHQQKALOSGPPQSRK 579

RESULT 13  
US-09-735-705-176  
; Sequence 176, Application US/09735705  
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaltanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-176

Query Match 100.0%; Score 2956; DB 21; Length 579;  
Best Local Similarity 100.0%; Pred. No. 8.6e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSGK 60  
|||||  
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMALKAIEALSGK 60  
QY 61 IELHGKPIEVESHVPRKRIKLOIRNIPHLQWEVLDLSLVQGVVSECEQVNTDSETA 120  
|||||  
DB 61 IELHGKPIEVESHVPRKRIKLOIRNIPHLQWEVLDLSLVQGVVSECEQVNTDSETA 120  
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRLGGRSS 180  
|||||  
DB 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRLGGRSS 180  
QY 161 ROGSGSVSKORPCDPLRLVPTQFVGAILGKAGATIRNITKOTOSKIDVHKKENAGAA 240  
|||||  
DB 161 ROGSGSVSKORPCDPLRLVPTQFVGAILGKAGATIRNITKOTOSKIDVHKKENAGAA 240  
QY 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEELPLKILAHNNVGLIKKEGRNLK 300  
|||||  
DB 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEELPLKILAHNNVGLIKKEGRNLK 300  
QY 301 KIEODTDRKTIISPLQELTLYNPERTITVKGAVETCAKAEELMKKIRESEYENDIASMNL 360  
|||||  
DB 301 KIEODTDRKTIISPLQELTLYNPERTITVKGAVETCAKAEELMKKIRESEYENDIASMNL 360  
QY 361 QAHILPGILNALGLFPTSGMPPTSGPPSAMPPIPOEEOSETETVHOFIPALSVGAI 420  
|||||  
DB 361 QAHILPGILNALGLFPTSGMPPTSGPPSAMPPIPOEEOSETETVHOFIPALSVGAI 420



Db 481 SPKEVWLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVVPDDTDPDENDQVVVKIT 540

OY 541 GHFYACVAGRKIOEILTOVKOHOOOKALQSGPPQSRK 579

Db 541 GHFYACVAGRKIOEILTOVKOHOOOKALQSGPPQSRK 579

Search completed: April 16, 2003, 16:29:56  
Job time : 390.852 secs





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Page 1

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:21:35 ; Search time 43.734 Seconds

(without alignments)  
1001.062 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 2956

Sequence: 1 MNKLYIGLSNAPSDLES.....VKHQOQKALQSGPQSRK 579

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2956	100.0	579	10	US-09-735-705-176
2	2956	100.0	579	10	US-09-850-716A-176
3	2956	100.0	579	10	US-09-897-778-176
4	2943	99.6	579	10	US-09-735-705-348
5	2943	99.6	579	10	US-09-850-716A-348
6	2943	99.6	579	10	US-09-897-778-348
7	2943	99.6	579	10	US-09-897-778-446
8	2943	99.6	579	10	US-09-897-778-449
9	2938	99.4	586	10	US-09-850-716A-427
10	2938	99.4	586	10	US-09-897-778-427
11	2190	74.1	577	10	US-09-873-637-2
12	1946.5	65.8	620	10	US-09-764-864-1116
13	949	32.1	261	10	US-09-764-864-1114
14	919	31.1	250	10	US-09-764-864-1532
15	636	21.2	171	10	US-09-764-864-1119
16	527	17.8	192	10	US-09-764-864-1117
17	474	16.0	93	10	US-09-864-761-48606
18	402	13.6	171	10	US-09-764-864-1536
19	238	8.1	49	10	US-09-873-637-22

20	237	8.0	48	10	US-09-873-637-24	Sequence 24, Appl
21	232	7.8	49	10	US-09-873-637-18	Sequence 18, Appl
22	227	7.7	45	10	US-09-864-761-45987	Sequence 45987, A
23	227	7.7	47	10	US-09-873-637-23	Sequence 23, Appl
24	225	7.6	47	10	US-09-873-637-21	Sequence 21, Appl
25	219	7.4	48	10	US-09-873-637-20	Sequence 20, Appl
26	218	7.4	47	10	US-09-873-637-17	Sequence 17, Appl
27	190	6.4	47	10	US-09-873-637-19	Sequence 19, Appl
28	187	6.3	465	10	US-09-925-301-1198	Sequence 1198, Ap
29	171	5.8	37	10	US-09-764-864-1534	Sequence 1534, Ap
30	141	4.8	359	9	US-10-025-367-25	Sequence 25, Appl
31	139.5	4.7	1179	9	US-09-821-883-29	Sequence 29, Appl
32	135.5	4.6	359	9	US-10-025-367-23	Sequence 23, Appl
33	134.5	4.6	337	9	US-10-025-367-27	Sequence 27, Appl
34	133	4.5	380	9	US-10-025-367-27	Sequence 27, Appl
35	132	4.5	201	10	US-09-764-864-1113	Sequence 1113, Ap
36	131.5	4.4	279	12	US-10-014-927-19	Sequence 19, Appl
37	130	4.4	633	10	US-09-821-687-10	Sequence 10, Appl
38	129.5	4.4	545	10	US-09-925-300-1415	Sequence 1415, Ap
39	128.5	4.4	579	10	US-09-821-687-4	Sequence 4, Appl1
40	128.5	4.3	561	10	US-09-925-300-1620	Sequence 1620, Ap
41	125.5	4.2	1601	10	US-09-862-027-40	Sequence 40, Appl
42	124	4.2	366	9	US-10-029-180-66	Sequence 66, Appl
43	123.5	4.1	915	9	US-10-029-180-74	Sequence 74, Appl
44	121.5	4.1	261	9	US-10-043-487-220	Sequence 220, Appl
45	120	4.1	261	9	US-10-043-487-220	Sequence 220, Appl

#### ALIGNMENTS

RESULT 1  
US-09-735-705-176  
Sequence 176, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Banquer, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-176

Query Match 100.0%; Score 2956; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 9,7e-218;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGLSNAPSDLESIFKDKATIPVSGPIVKTGYAFVDCPDSESMALKATEALSGK 60  
DB 1 MNKLYIGLSNAPSDLESIFKDKATIPVSGPIVKTGYAFVDCPDSESMALKATEALSGK 60  
QY 61 IELHCKPIEVHSPVKQRIRKQIRNIPPHLQWELVDSLLVQGVNESCQVNTDSETA 120  
DB 61 IELHCKPIEVHSPVKQRIRKQIRNIPPHLQWELVDSLLVQGVNESCQVNTDSETA 120

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OY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNLOOPRGRGLGGRSS 180
DB 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNLOOPRGRGLGGRSS 180
OY 181 ROGSPGSVSKOKPCDPLRLVLPVTOFGAIIKGEAGATIRNTKOTOSKIDVHRKENAGAA 240
DB 181 ROGSPGSVSKOKPCDPLRLVLPVTOFGAIIKGEAGATIRNTKOTOSKIDVHRKENAGAA 240
OY 241 EKSTITLSTPEGSTSAACKSTLEIMHKEADIKFTEEPILKILANNNVGLGKESRNLK 300
DB 241 EKSTITLSTPEGSTSAACKSTLEIMHKEADIKFTEEPILKILANNNVGLGKESRNLK 300
OY 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETCAKAEIEIMKIRESEYENDIASMNL 360
DB 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETCAKAEIEIMKIRESEYENDIASMNL 360
OY 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
DB 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVITGPPEAOFKAGRIYKIKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVITGPPEAOFKAGRIYKIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVELONLSAEVVPVPRDQTPDENOVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVELONLSAEVVPVPRDQTPDENOVVVKIT 540
OY 541 GHFYACQVAAKRIQEIITOVKHOQOKALOGSPQSRK 579
DB 541 GHFYACQVAAKRIQEIITOVKHOQOKALOGSPQSRK 579

RESULT 2
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US2002015139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: RETIERS, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match 100.0%; Score 2956; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.7e-218;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 241 EKSTITLSTPEGSTSAACKSTLEIMHKEADIKFTEEPILKILANNNVGLGKESRNLK 300
DB 241 EKSTITLSTPEGSTSAACKSTLEIMHKEADIKFTEEPILKILANNNVGLGKESRNLK 300
OY 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETCAKAEIEIMKIRESEYENDIASMNL 360
DB 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETCAKAEIEIMKIRESEYENDIASMNL 360
OY 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
DB 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVITGPPEAOFKAGRIYKIKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVITGPPEAOFKAGRIYKIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVELONLSAEVVPVPRDQTPDENOVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVELONLSAEVVPVPRDQTPDENOVVVKIT 540
OY 541 GHFYACQVAAKRIQEIITOVKHOQOKALOGSPQSRK 579
DB 541 GHFYACQVAAKRIQEIITOVKHOQOKALOGSPQSRK 579

RESULT 3
US-09-897-778-176
: Sequence 176, Application US/09897778
: Patent No. US2002014713A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-176

Query Match 100.0%; Score 2956; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.7e-218;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLICKEGRNK 300
DB 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLICKEGRNK 300
QY 301 KIEODTDKRTITISPLQELTYNPERTIYKGVNETCAKAEELIMKKITRESEYENDIASMNL 360
DB 301 KIEODTDKRTITISPLQELTYNPERTIYKGVNETCAKAEELIMKKITRESEYENDIASMNL 360
QY 361 QAHILPGNLNALGLFPPTSGMPPPTSGPPSAMPPYPQFQSETEETHOIFALSVGAI 420
DB 361 QAHILPGNLNALGLFPPTSGMPPPTSGPPSAMPPYPQFQSETEETHOIFALSVGAI 420
QY 421 IKGOGOHKOLSRFAGASIKIAPAEAPDAKVMVITITGPPFAOKRAGRIYGIKEENY 480
DB 421 IKGOGOHKOLSRFAGASIKIAPAEAPDAKVMVITITGPPFAOKRAGRIYGIKEENY 480
QY 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDPTPDENDQVYVKIT 540
DB 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDPTPDENDQVYVKIT 540
QY 541 GHFYACQVAKRKIOEILTYVKOHQOQKALQSGPPQSRK 579
DB 541 GHFYACQVAKRKIOEILTYVKOHQOQKALQSGPPQSRK 579

```

## RESULT 4

```

US-09-735-705-348
: Sequence 348, Application US/09735705
: Patent No. US2002005229A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Ligu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-348

```

Query Match 99.6%; Score 2943; DB 10; Length 579;

Best Local Similarity 99.7%; Pred. No. 9,6e-217;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
QY 61 IELHCKPIEVEHSVPKQRIRKIQIRNIPPHLOMEYLDLSLYOGVVESECOVNTDSE7A 120
DB 61 IELHCKPIEVEHSVPKQRIRKIQIRNIPPHLOMEYLDLSLYOGVVESECOVNTDSE7A 120
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180
DB 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180
QY 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAIIEGATIRNITKQOSKIDVHRKENAGAA 240
DB 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAIIEGATIRNITKQOSKIDVHRKENAGAA 240

```

```

DB 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAIIEGATIRNITKQOSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLICKEGRNK 300
DB 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLICKEGRNK 300
QY 301 KIEODTDKRTITISPLQELTYNPERTIYKGVNETCAKAEELIMKKITRESEYENDIASMNL 360
DB 301 KIEODTDKRTITISPLQELTYNPERTIYKGVNETCAKAEELIMKKITRESEYENDIASMNL 360
QY 361 QAHILPGNLNALGLFPPTSGMPPPTSGPPSAMPPYPQFQSETEETHOIFALSVGAI 420
DB 361 QAHILPGNLNALGLFPPTSGMPPPTSGPPSAMPPYPQFQSETEETHOIFALSVGAI 420
QY 421 IKGOGOHKOLSRFAGASIKIAPAEAPDAKVMVITITGPPFAOKRAGRIYGIKEENY 480
DB 421 IKGOGOHKOLSRFAGASIKIAPAEAPDAKVMVITITGPPFAOKRAGRIYGIKEENY 480
QY 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDPTPDENDQVYVKIT 540
DB 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDPTPDENDQVYVKIT 540
QY 541 GHFYACQVAKRKIOEILTYVKOHQOQKALQSGPPQSRK 579
DB 541 GHFYACQVAKRKIOEILTYVKOHQOQKALQSGPPQSRK 579

```

## RESULT 5

```

US-09-850-716A-348
: Sequence 348, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Relfer, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-348

```

Query Match 99.6%; Score 2943; DB 10; Length 579;

Best Local Similarity 99.7%; Pred. No. 9,6e-217;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
QY 61 IELHCKPIEVEHSVPKQRIRKIQIRNIPPHLOMEYLDLSLYOGVVESECOVNTDSE7A 120
DB 61 IELHCKPIEVEHSVPKQRIRKIQIRNIPPHLOMEYLDLSLYOGVVESECOVNTDSE7A 120
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180
DB 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180
QY 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAIIEGATIRNITKQOSKIDVHRKENAGAA 240
DB 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAIIEGATIRNITKQOSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLICKEGRNK 300
DB 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLICKEGRNK 300
QY 301 KIEODTDKRTITISPLQELTYNPERTIYKGVNETCAKAEELIMKKITRESEYENDIASMNL 360
DB 301 KIEODTDKRTITISPLQELTYNPERTIYKGVNETCAKAEELIMKKITRESEYENDIASMNL 360

```

```
Db 301 KIEODTDRKITISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Qy 361 QAHLIPGLNALGLPPTSGMPPTSGPPSAMTPPYPOESETETVHOFIPALSVGAI 420
Db 361 QAHLIPGLNALGLPPTSGMPPTSGPPSAMTPPYPOESETETVHOFIPALSVGAI 420
Qy 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAQGRITGKIEENY 480
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAQGRITGKIEENY 480
Qy 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Db 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Qy 541 GHFYACOVAORKIOELITVYKHOQOKALOGSGPPQSRK 579
Db 541 GHFYACOVAORKIOELITVYKHOQOKALOGSGPPQSRK 579
```

## RESULT 6

```
US-09-897-778-348
: Sequence 348, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897.778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ NOS: 467
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-348
```

```
Query Match 99.6% Score 2943: DB 10: Length 579:
Best Local Similarity 99.7% Pred. No. 9.6e-217:
Matches 577: Conservative 0: Mismatches 2: Indels 0: Gaps 0:
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```
Qy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTGYAFVDCPDESMALKATEALSGK 60
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTGYAFVDCPDESMALKATEALSGK 60
Qy 61 IELHGKPLEVHSHVPRKORIRKLOIRNIPRLQWEVLDLSLOYGVVSCQVNTDSEFA 120
Db 61 IELHGKPLEVHSHVPRKORIRKLOIRNIPRLQWEVLDLSLOYGVVSCQVNTDSEFA 120
Qy 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAIYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Db 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAIYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Qy 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAITGKGCATINIRIKQOSKIDVHREKNAAGAA 240
Db 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAITGKGCATINIRIKQOSKIDVHREKNAAGAA 240
Qy 241 EKSITILSTPEGTSAAKSTILEIMKEADIKFTEELPKLIHANNFVGRIGEGRNILK 300
Db 241 EKSITILSTPEGTSAAKSTILEIMKEADIKFTEELPKLIHANNFVGRIGEGRNILK 300
Qy 301 KIEODTDRKITISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Db 301 KIEODTDRKITISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
```

```
Db 301 KIEODTDRKITISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Qy 361 QAHLIPGLNALGLPPTSGMPPTSGPPSAMTPPYPOESETETVHOFIPALSVGAI 420
Db 361 QAHLIPGLNALGLPPTSGMPPTSGPPSAMTPPYPOESETETVHOFIPALSVGAI 420
Qy 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAQGRITGKIEENY 480
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAQGRITGKIEENY 480
Qy 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Db 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Qy 541 GHFYACOVAORKIOELITVYKHOQOKALOGSGPPQSRK 579
Db 541 GHFYACOVAORKIOELITVYKHOQOKALOGSGPPQSRK 579
```

## RESULT 7

```
US-09-897-778-446
: Sequence 446, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897.778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ NOS: 467
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 446
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-446
```

```
Query Match 99.6% Score 2943: DB 10: Length 579:
Best Local Similarity 99.7% Pred. No. 9.6e-217:
Matches 577: Conservative 0: Mismatches 2: Indels 0: Gaps 0:
```

```
Qy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTGYAFVDCPDESMALKATEALSGK 60
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTGYAFVDCPDESMALKATEALSGK 60
Qy 61 IELHGKPLEVHSHVPRKORIRKLOIRNIPRLQWEVLDLSLOYGVVSCQVNTDSEFA 120
Db 61 IELHGKPLEVHSHVPRKORIRKLOIRNIPRLQWEVLDLSLOYGVVSCQVNTDSEFA 120
Qy 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAIYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Db 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAIYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Qy 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAITGKGCATINIRIKQOSKIDVHREKNAAGAA 240
Db 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAITGKGCATINIRIKQOSKIDVHREKNAAGAA 240
Qy 241 EKSITILSTPEGTSAAKSTILEIMKEADIKFTEELPKLIHANNFVGRIGEGRNILK 300
Db 241 EKSITILSTPEGTSAAKSTILEIMKEADIKFTEELPKLIHANNFVGRIGEGRNILK 300
Qy 301 KIEODTDRKITISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Db 301 KIEODTDRKITISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
```



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Page 6

Oy	482 PEEVKELEAHIRPSPAAARVYKGGKTVELONLSSAAVVYPDPTDENDQVVKITG 54
Dd	489 PREVKLEAHLRVPSPAARVYKGGKTVELONLSSAAVVYPDQTPDENDDQVVKITG 548
Oy	542 HRYACQAQRKIQLIELITVKKHQOQKALSGPPQSRRK 579
Dd	549 HRYACQAQRKIQLILTVKKHQOQKALSGPPQSRRK 566

```

RESULT 10.
US-09-897-778-427
Sequence 427, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Manneakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshitiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 427
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-427

```

	Query Match Similarity	99.4%;	Score 2938;	DB 10;	Length 586;
	Best Local Similarity	99.7%;	Pred. No. 2,3e-216;		
	Matches 576;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	2	NKLYIENLSENAAPSDSEIFRDAKIPVAGPFLVKTGVAFVDCPDDESMALKAIEALSCKI	61		
DB	9	NKLYIENLSENAAPSDSEIFRDAKIPVAGPFLVKTGVAFVDCPDDESMALKAIEALSCKI	68		
QY	62	ELHGKRIEIEHSVPRKRIKRLIRIPIPHLOMEVLSLLVOYGVESECVNTDSEFV	121		
DB	69	ELHGKRIEIEHSVPRKRIKRLIRIPIPHLOMEVLSLLVOYGVESECVNTDSEFV	128		
QY	122	VVNTYSKKQAQALIDLNGFOLENTLLVVYIPDMAAQNPLQOPRGRRLGGRSSR	181		
DB	129	VVNTYSKKQAQALIDLNGFOLENTLLVVYIPDMAAQNPLQOPRGRRLGGRSSR	188		
QY	182	QSGPSGVSKORCPCLPRLLVPOFGALITGEGASTIRNTTKTQSGKIDVHKEMAGAAE	241		
DB	189	QSGPSGVSKORCPCLPRLLVPOFGALITGEGASTIRNTTKTQSGKIDVHKEMAGAAE	248		
QY	242	KSTITLSPPEGSAAKSLIEIMHKRAODIKTEPIPLKILANNVVGSLTCKEERNLKK	301		
DB	249	KSTITLSPPEGSAAKSLIEIMHKRAODIKTEPIPLKILANNVVGSLTCKEERNLKK	308		
QY	302	IEDDDYTKITLSPLOEITLXNPKRTITVYGVNVEYCAKAAEELIMKRTIESTENDIASMLQ	361		
DB	309	IEDDDYTKITLSPLOEITLXNPKRTITVYGVNVEYCAKAAEELIMKRTIESTENDIASMLQ	368		
QY	362	AMILPELINALGLPEPTSGMPPTISGPPSANTPPYPOFEOSETETVHOFPDALSVCATII	421		
DB	369	AMILPELINALGLPEPTSGMPPTISGPPSANTPPYPOFEOSETETVHOFPDALSVCATII	428		
QY	422	GKGGGHIKQLSFPAGASIKIAPAEADAVRVVITITGPEAKRAGRIYGIKKEENFVS	481		
DB	429	GKGGGHIKQLSFPAGASIKIAPAEADAVRVVITITGPEAKRAGRIYGIKKEENFVS	488		

QY	Db	QY	Db
482	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	542	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
483	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	543	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
484	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	544	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
485	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	545	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
486	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	546	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
487	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	547	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
488	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	548	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
489	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	549	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
490	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	550	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
491	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	551	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
492	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	552	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
493	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	553	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
494	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	554	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
495	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	555	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
496	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	556	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
497	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	557	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
498	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	558	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
499	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	559	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK
500	PEEEKLEAAHRYPSPAACRVYKGGGTVEIQLNLSAAEVVPDQTPDENQVAVKTTG	560	HEVACVAQRKIQEILITVYKQHQDQKALQSGPPQSRK

```

RESULT 11
US-09-873-637-2
Sequence 2, Application US/09873637
Patent No. US20020061543A1
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/873,637
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ. ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO. 2
LENGTH: 577
TYPE: PRT
ORGANISM: Mus musculus
US-09-873-637-2

```

Query Match	Score	2190:	DB	10:	Length	577:
Best Local Similarity	74.1%:	Pred. No.	3.3e-159:			
Matches	434:	Conservative	62:	Mismatches	74:	Indels
					16:	Gaps
QY	1	MKRLVLTGNLENNAPASDSEJFIKDAKIPVSGPFLVTKGVAFNAPDCDESMALKKIAEISLGR	60	1	1	1
Db	1	MKRLVLTGNLENNESVTPADLEKVFKAHKIISVSGPFLVKSQVAFNDCDEDEHMAKIAIEFSGR	60	1	1	1
QY	61	IELHAKPLIEVHSHVPRRORIRKLOTRINPPLHWEVDSILVQYGVSSCPVONTSEFA	120	1	1	1
Db	61	VELQGRKLREHSHVPRKQSRKRIQIRINPPLQREVEIDSLVQYGVENCOYVNTSEFA	120	1	1	1
QY	121	VVNTVYSSKQQAQALDKLNGFOLNEFTLKVAVYIPDEMAQOQPLQDGRGR--GLGORS	179	1	1	1
Db	121	VVNTVYSNRQDTQALMKLNGHOLENHALKVSYIPDQIQY---GPRNGRQFGPSRQO	176	1	1	1
QY	180	SHQSP---GSVSKKPCDDPLRLVLPQFVAIIIGEGATIRNTKQTQSKIDVHRKN	236	1	1	1
Db	177	PROGSPVAQAAPAKQDPYDILRLVLPQYGAIIIGEGATIRNTKQTQSKIDVHRKN	236	1	1	1
QY	237	AAAEKSTITLSPRESTSAACKSTLEIMKEMADIKTEIEPIKLAIANNVGLLGRKG	296	1	1	1
Db	237	AAAPAKIAVSHSTPEGSCSACKMILEIMKEMAKDTKADVPLKLAIANNVGLLGRKG	296	1	1	1
QY	297	RALKTIKODPDPIKTIISPLQSLTIYMPERTITVGNVENCARAEELIMKKIRASYENDVA	356	1	1	1
Db	297	RALKTVKQDIEFKTIISLQDLTIYMPERTITVGCALENCRADEIMKKIRAEYENDVA	356	1	1	1
QY	357	SMNLQALITGCLNALGLPSPSGMPPRTQSPSMT--PRYQFQDS--ETVYHQFIP	413	1	1	1
Db	357	AMSLDHLITGCLNALVGLFPASSAVPP---PSSVTGAAPRSFQAPQDEMVOVFIP	413	1	1	1
QY	414	ALSVGATIIIGQGHITQKLSRPRAGSKITKAPAPADAVAPVYIITGPAPQKQKQITVK	473	1	1	1
Db	414	ADQVATIIIGKRGHITQKLSRPRASIKTAPETPDQSKRVAVYITGPAPQKQKQITVK	473	1	1	1
QY	474	TEENFVSPKEEVKLEAHIRPSPAGKVIIGCKGTVELQNLSSAEVYVYPRQOTDEMD	533	1	1	1
Db	474	LEENFVSPKEEVKLETHIRPSPAGKVIIGGGVTVNELQNLTALEVYVYPRQOTDEMD	533	1	1	1
QY	534	OVVAVITGHFYACQVAKRIDEITLYVQKHQDQKALQSGFQSRRK	579	1	1	1
Db	534	OVVAVITGHFYASQMAKRIIDYIAQKQ-QHQKQ--QSNIAQKRI	577	1	1	1

```

RESULT 12
US-09-764-864-1116
; Sequence 1116, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1116
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (533)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1116

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Query Match          65.8%; Score 1946.5; DB 10; Length 620;
Best Local Similarity 65.1%; Pred. No. 1.5e-140;
Matches 385; Conservative 81; Mismatches 96; Indels 29; Gaps 8;

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OY 1 MNKLYIGNLSENPAPSDLESIFKDAKIPVSGPLVGTGAFVDCPDSEWALKAIEALSGK 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 23 MNKLYIGNLSPAVTADLRKLFGRKPLPLAGVLLKSGYAFADYDPQNNATIAITLSGK 82
OY 61 IELGKPLEVSHVPRQRKRLQIRNIPPHLOWEYLDLSLOYGVESCEOVNTDSETA 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 83 VELHCKIWEVSYSKRLRSKRLQIRNIPPHLOWEYLDLSLOYGVENVDGNTDETA 142
OY 121 VVNTYSSKQDARQALDKINGFQLENTFLKAVIIPDEMAQONPQOQPRGRGLGQRRSS 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 143 VVNTYATREAKTAMKLSGHOPEYTFKISTIPDEYSSPSPP--RAQR--GDHSR 198
OY 181 ROG-SPGSVKOKPCDLPRLRLVPTQFVCAITGEGATIRNTKOTOSKIDVHRKENAGA 239
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 199 EGNHAPGGSQARQIDPPLRLVPTQFVCAITGEGATIRNTKOTOSKIDVHRKENAGA 258
OY 240 AEKSTILSPGTSACKSILEIMHKEADIKTEIEPLKILAHNPFGRILIGEGNLT 299
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 259 AEKPTTHATPEGTSEACRMILEIMHKEADIKTEIEPLKILAHNPFGRILIGEGNLT 318
OY 300 KKEODDTTKITISPLQELTLYNPERTITVGNVETCANAEEMKIKIRESENDIASMN 359
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 319 KKEHETGKTITISLQDLSTYNERITVKGIVEACASAEIEMKIKLEAFENMLAVN 378
OY 360 LOAHILPOLNINLGLF-----PPTS--GMPPPT-----SGPPSAMTP-----P 396
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 379 QOANLIPOLNINLGLFSTGLSVLSPAGPRGAPAPAPHPFTTHGSSLYPHHOGEP 438
OY 397 YPOFQO--SETETVHOFTPALSGVAILIGKOGHITKOLSRFAGASIKIAPAEADAVRWYI 455
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 439 FPHHISTYDEQETVNLFTPLQAVGAILIKKGAHITKOLARRAGASIKIAPAEADAVRWYI 498
OY 456 ITGPEPAQFAQGRIRYKIKRENFVSPKEEVKLEAHIRVPSFAAGVIGKGTAVNELON 515
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 499 ITGPEPAQFAQGRIRYKIKRENFVSPKEEVKLEAHIRVPSFAAGVIGKGTAVNELON 558
OY 516 LSSAVVVPDQTPDENDDVVYKITGHFYACQVAKRIQELITLVYQHQOO 566
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 559 LTSAEVLPDQTPDENDDVVYKITGHFYACQVAKRIQELITLVYQHQOO 609

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RESULT 13
US-09-764-864-1114
; Sequence 1114, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1114
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1114

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Query Match          32.1%; Score 949; DB 10; Length 261;
Best Local Similarity 74.5%; Pred. No. 6.9e-65;
Matches 193; Conservative 26; Mismatches 32; Indels 8; Gaps 5;

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OY 324 ERTIVKGNVETCAKAEIEIKKIRESENDIASMNLOAHILPOLNINLGLFPPTSGMP 383
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 8 ERTIVKGAIEGCCRAEIEIKKIRESENDIASMNLOAHILPOLNINLGLFPPTSGMP 67
OY 384 PPTSGPPSAMT--PPYPOFQO--SETETVHOFTPALSGVAILIGKOGHITKOLSRFAGASIK 440
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 68 PP---PPSSVTGAARYSFPQAPDEMYVITPAQVGAITIGKGRHITKOLSRFAGASIK 124
OY 441 IAPAEAPDAKVMVITITGPEPAQFAQGRIRYKIKRENFVSPKEEVKLEAHIRVPSFAAG 500
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 125 IAPETPDSKVMVITITGPEPAQFAQGRIRYKIKRENFVSPKEEVKLEAHIRVPSFAAG 184
OY 501 RYIGKGTAVNELONLSSAEVVPDQTPDENDDVVYKITGHFYACQVAKRIQELITLVY 560
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 185 RYIGKGTAVNELONLSSAEVVPDQTPDENDDVVYKITGHFYACQVAKRIQELITLVY 244
OY 561 KOHQOQKALQSGPPQSRK 579
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 245 KO-QHQKG-QSNQQAARRK 261

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RESULT 14
US-09-764-864-1532
; Sequence 1532, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1532
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (134)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1532

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```

Query Match          31.1%; Score 919; DB 10; Length 250;
Best Local Similarity 73.3%; Pred. No. 1.3e-62;
Matches 187; Conservative 26; Mismatches 34; Indels 8; Gaps 5;

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OY 328 TVKGNVETCAKAEIEIKKIRESENDIASMNLOAHILPOLNINLGLFPPTSGMPPTS 387
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 TVKGAIEGCCRAEIEIKKIRESENDIASMNLOAHILPOLNINLGLFPPTSGMPPTS 58

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OY 388 GPPSAMT--PPYPOFEO--ETETVHOFIPALSGATIGKOGHOKOLSRFAGASIKRIAPA 444
DB 59 -PPSSVTGAAPYSSFMQAPDEQEMQVFLPAQVCAIIGKKGHOKOLSRFASASIKRIAPP 117
OY 445 EAPDAKRVYIITGPPEOQFAKGRITGKIKEENFVSPKEEVKLEAHIRVPSFAAGRVIG 504
DB 118 ETPDSKVRXIIITGPXAKQFAKGRITGKIKEENFVSPKEEVKLEAHIRVPSAAGRVIG 177
OY 505 KGGKTVNELQNLSSAEVVVPRDQTPDENDDQVVKITGHFYACQVAKRKIOETITGVKOHQ 564
DB 178 KGGKTVNELQNLSSAEVVVPRDQTPDENDDQVVKITGHFYASQMAQRKIRIDILAQVKQ-Q 236
OY 565 QOKALQSGPPOSRRK 579
DB 237 HOKG-QSNOQAARK 250
```

```
RESULT 15
US-09-764-864-1119
; Sequence 1119, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; PUBLICATION DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1119
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1119
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Query Match 21.2%; Score 626; DB 10; Length 171;
Best Local Similarity 80.5%; Pred. No. 1.8e-40;
Matches 120; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
```

```
OY 418 GAIGKOGHOKOLSRFAGASIKRIAPAEAPDAKRVYIITGPPEOQFAKGRITGKIKEE 477
DB 12 GAIGKKGHOKOLSRFAGASIKRIAPAEAPDAKRVYIITGPPEOQFAKGRITGKIKEE 71
OY 478 NFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDDQV 537
DB 72 NFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDDQV 131
OY 538 KITGHFYACQVAKRKIOETITGVKOHQ 566
DB 132 KITGHFYACQVAKRKIOETITGVKOHQ 160
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Search completed: April 16, 2003, 16:32:11  
Job time : 45.734 secs



OM protein -protein search, using sw model  
Run on: April 16, 2003, 16:19:55 ; Search time 71.3054 Seconds  
(without alignments)  
1266.170 Million cell updates/second

Title: US-09-897-778-176  
Perfect score: 2956  
Sequence: 1 MNKDYIGNLSENAPSDLES.....VKQHQQKALQSGPPQSRRK 579

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 705215 seqs, 155932251 residues

Total number of hits satisfying chosen parameters: 705215

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Pending_Patents_AA-New:*
1 : /cgn2_6.ptiddata/1/paa/PCU_NEW_COMB.pep.*
2 : /cgn2_6.ptiddata/1/paa/US07_NEW_COMB.pep.*
3 : /cgn2_6.ptiddata/1/paa/US07_NEW_COMB.pep.*
4 : /cgn2_6.ptiddata/1/paa/US09_NEW_COMB.pep.*
5 : /cgn2_6.ptiddata/1/paa/US09_NEW_COMB.pep.*
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7 : /cgn2_6.ptiddata/1/paa/US10_NEW_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query				Description	
No.	Score	Match	Length	DB	ID		
1	2956	100.0	579	6	US-10-313-986-176	Sequence 176,	App1
2	2956	100.0	579	6	US-10-348-113-9-255	Sequence 255,	App1
3	2943	99.6	579	6	US-10-313-986-348	Sequence 348,	App1
4	2943	99.6	579	6	US-10-313-986-446	Sequence 446,	App1
5	2943	99.6	579	6	US-10-313-986-449	Sequence 449,	App1
6	2943	99.6	579	6	US-10-313-986-480	Sequence 480,	App1
7	2943	99.6	586	6	US-10-313-986-486	Sequence 486,	App1
8	2938	99.4	586	6	US-10-313-986-427	Sequence 427,	App1
9	2937	99.4	579	6	US-10-313-986-484	Sequence 484,	App1
10	2826	95.6	558	5	US-09-124-676-92918	Sequence 92918,	App1
11	2826	95.6	558	5	US-09-124-676-92918	Sequence 92918,	App1
12	2459.5	83.2	492	5	US-09-124-676-92916	Sequence 92916,	App1
13	2459.5	83.2	492	5	US-09-124-676-92916	Sequence 92916,	App1
14	2191	71.1	577	6	US-10-313-986-500	Sequence 500,	App1
15	2112	71.4	572	5	US-09-124-676-48617	Sequence 48617,	App1
16	2112	71.4	572	5	US-09-124-676-48618	Sequence 48618,	App1
17	2112	71.4	572	5	US-09-124-676-48617	Sequence 48617,	App1
18	2112	71.4	572	5	US-09-124-676-48618	Sequence 48618,	App1
19	2105.5	71.2	602	5	US-09-124-676-48619	Sequence 48619,	App1
20	2105.5	71.2	602	5	US-09-124-676-48620	Sequence 48620,	App1
21	2105.5	71.2	602	5	US-09-124-676-48619	Sequence 48619,	App1
22	2105.5	71.2	602	5	US-09-124-676-48620	Sequence 48620,	App1
23	2089	70.7	598	5	US-09-124-676-48616	Sequence 48616,	App1
24	2089	70.7	598	5	US-09-124-676-48621	Sequence 48621,	App1
25	2089	70.7	598	5	US-09-124-676-48616	Sequence 48616,	App1
26	2089	70.7	598	5	US-09-124-676-48621	Sequence 48621,	App1

27	1950.5	66.0	501	587	6	US-10-313-986-501	Sequence 501, App
28	1944.5	65.8	599	7	US-60-453-131-11537	A Sequence 11527, A	
29	1944.5	65.8	599	7	US-60-453-131-11537	A Sequence 11527, A	
30	1944.5	65.8	599	7	US-60-453-131-11537	A Sequence 11527, A	
31	1862	63.0	40	11528	4	US-60-453-050-11528	A Sequence 11528, A
32	1862	63.0	40	11528	4	US-60-453-050-11528	A Sequence 11528, A
33	1703.5	57.6	555	7	PCT-US02-31357-40	Sequence 40, Appl	
34	1703.5	57.6	555	7	US-10-262-445-40	Sequence 40, Appl	
35	1403.6	35.0	219	7	US-60-453-135-7694	Sequence 7694, Appl	
36	1036	35.0	219	7	US-60-453-050-7694	Sequence 7694, Appl	
37	710.5	24.0	255	7	US-60-453-680-15601	Sequence 15601, A	
38	690	23.3	134	5	US-09-724-6756-92917	Sequence 92917, A	
39	572.5	19.4	187	7	US-09-724-6756-92917	Sequence 92917, A	
40	572.5	19.4	187	7	US-60-453-680-12976	A Sequence 12976, A	
41	572.5	19.4	187	7	US-60-453-050-8175	Sequence 8175, App	
42	405	13.7	80	6	US-10-313-986-475	Sequence 475, App	
43	405	13.7	80	6	US-10-313-986-475	Sequence 475, App	
44	360	12.2	70	6	US-10-313-986-475	Sequence 475, App	
45	357	12.1	70	6	US-10-313-986-471	Sequence 471, App	

## ALIGNMENTS

```

RESULT 1
US-10-313-986-176
: Sequence 176, Application US/10313986
: GENERAL INFORMATION:
: APPLICANT: Fey, Teresa M.
: APPLICANT: McNabb, Andria
: APPLICANT: Matsubae, Yoshihito
: APPLICANT: Reed, Steven G.
: APPLICANT: Wang, Tsongting
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455c19
: CURRENT APPLICATION NUMBER: US/10/313, 986
: CURRENT FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 560
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-313-986-176

```

Query Match	100.0%;	Score 2956;	DB 6;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 4e-244;		
Matches 579;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

1	MMKLITGLSNNAPSDLESIRKDAKIPYSGPELTKYGFVYCCPESMAKALAEALSG	60
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93	1	
94	1	
95	1	
96	1	
97	1	
98	1	
99	1	
100	1	

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Page 2

QY	361	QAHILGJLNLNLLGPEPTSGMPPTSGPSPAMPPVPOPEOSTETVHOETPALSVAI	420
Db	361	QAHILGJLNLNLLGPEPTSGMPPTSGPSPAMPPVPOPEOSTETVHOETPALSVAI	420
QY	421	IGKOGCHTQOLSRFAGSASTKIAPAEAPDAKVMVITTGPEBAQKAGRIYKIKEENFV	480
Db	421	IGKOGCHTQOLSRFAGSASTKIAPAEAPDAKVMVITTGPEBAQKAGRIYKIKEENFV	480
QY	481	SEPEEYKLEAHIRVPSFAGRVITGKGKTVNELNLSAEVYVPRDQTDENDQYVVKIT	540
Db	481	SEPEEYKLEAHIRVPSFAGRVITGKGKTVNELNLSAEVYVPRDQTDENDQYVVKIT	540
QY	541	GHEFYACVAQRKIQEILTOYKQHQOQKALÖSSPSPSRK	579
Db	541	GHEFYACVAQRKIQEILTOYKQHQOQKALÖSSPSPSRK	579

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RESULT 2
US-10-348-119-255
: Sequence 255, Application US/10348119
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
: TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES
: TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
: FILE REFERENCE: D0185 NP
: CURRENT APPLICATION NUMBER: US/10/348.119
: CURRENT FILING DATE: 2003-01-17
: PRIOR APPLICATION NUMBER: US 60/350,061
: PRIOR FILING DATE: 2002-01-18
: NUMBER OF SEQ ID NOS: 795
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 255
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-348-119-255

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Query Match	100.0%	Score 2956	DB 6	Length 579
Best Local Similarity	100.0%	Pred. No. 4e-244		
Matches 579	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MNKLTYGNLSENAAPSDLESTIFKDAKIPVSGFELTKGTVAFCVCCPSNALKATIAISGK	60	
Db	1	MNKLTYGNLSENAAPSDLESTIFKDAKIPVSGFELTKGTVAFCVCCPSNALKATIAISGK	60	
QY	61	IELHGKPIFEVSEVSPKRORIKLOIRNIPPHOMVEUDLSLVOYGAVESCEQVNFNDSTA	120	
Db	61	IELHGKPIFEVSEVSPKRORIKLOIRNIPPHOMVEUDLSLVOYGAVESCEQVNFNDSTA	120	
QY	121	VVVVTVSSKDOARALNKLNGFOLNFTLKVAYIIDEKAAQNPLOQPGRGRLGQORSS	180	
Db	121	VVVVTVSSKDOARALNKLNGFOLNFTLKVAYIIDEKAAQNPLOQPGRGRLGQORSS	180	
QY	181	QQSPSPSVSKOPDDLRLRLVPTQEVGAIICKEGATIRNITQOTSKIDVHRKKNAAGA	240	
Db	181	QQSPSPSVSKOPDDLRLRLVPTQEVGAIICKEGATIRNITQOTSKIDVHRKKNAAGA	240	
QY	241	EKSITTLSPGEGTSAACKSILEIMHKEADODIFTEBEIPEKLIHANNFVGRILGKGRMLK	300	
Db	241	EKSITTLSPGEGTSAACKSILEIMHKEADODIFTEBEIPEKLIHANNFVGRILGKGRMLK	300	
QY	301	KIEODPDKIRITISPLQELTYLNPERTITVKGAVETCAAAEELIMKKIRSESYNDIASNML	360	
Db	301	KIEODPDKIRITISPLQELTYLNPERTITVKGAVETCAAAEELIMKKIRSESYNDIASNML	360	
QY	361	QAHLIPGINTLALALFPPITSGMPPTSGSPASAMPVPVPOFQOSEETVYHOQIPALSYGAI	420	
Db	361	QAHLIPGINTLALALFPPITSGMPPTSGSPASAMPVPVPOFQOSEETVYHOQIPALSYGAI	420	
QY	421	ICKGCHGKIKOLSRFAGASIKIAPAEAPDAKVMVYITGPEAOPKAGGRIYIKIKEENFV	480	
Db	421	ICKGCHGKIKOLSRFAGASIKIAPAEAPDAKVMVYITGPEAOPKAGGRIYIKIKEENFV	480	

Db	421	IKGQGNHKKQLSFRFASAKIAPAEADAVVRVILITSPBAOKKADGRITYKILEENFV	4808
QY	481	SKREVEVKLEAHIVPSPFAGAGYIKGGKVTNELJONLSASAEVVRPQDTDEDDQVVAIT	5400
Db	481	SKREVEVKLEAHIVPSPFAGAGYIKGGKVTNELJONLSASAEVVRPQDTDEDDQVVAIT	5400
QY	541	GHFYACGVAAQRKIQELITLVYVHOHQOKALQSGPQSRK	579
Db	541	GHFYACGVAAQRKIQELITLVYVHOHQOKALQSGPQSRK	579

```

? RESULT 3
? US-10-313-986-348
? Sequence 348, Application US/10313986
? GENERAL INFORMATION:
? APPLICANT: Foy, Teresa M.
? APPLICANT: McNabb, Andrea
? APPLICANT: Watanabe, Yoshihiro
? APPLICANT: Reed, Steven G.
? APPLICANT: Wang, Tongtong
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? FILE REFERENCE: 210121.453C19
? CURRENT APPLICATION NUMBER: US/10/313,986
? CURRENT FILING DATE: 12-04
? NUMBER OF SEQ ID NOS: 560
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 348
? LENGTH: 579
? TYPE: prt
? ORGANISM: Homo sapiens
? US-10-313-986-348

```

Query Match	99.6%	Score 2943	DB 6.1	Length 579:
Best Local Similarity	99.7%	Ped. No. 5, 2e-243		
Matches 577:	Conservative	0	Mismatches 2:	Indels 0
			Gaps	0:
Qy	1	MMKLYIGNTSENAAPSDJESTIFPKDAIPVSPGPFLVKGAVFVDCDDSMALKKIEALSGK	60	
Db	1	MMKLYIGNTSENAAPSDJESTIFPKDAIPVSPGPFLVKGAVFVDCDDSMALKKIEALSGK	60	
Qy	61	IELGKPIEIVHSVSKRQRIKRIKJOINIPRHLOWEYJDELILVOYGWVESCEQVNDSTETA	120	
Db	61	IELGKPIEIVHSVSKRQRIKRIKJOINIPRHLOWEYJDELILVOYGWVESCEQVNDSTETA	120	
Qy	121	VVNTYSKKQKQARQALDKLNGFOLNFYTLKAAVITPEDMAAQNPADQPRCRRRLGQRSS	180	
Db	121	VVNTYSKKQKQARQALDKLNGFOLNFYTLKAAVITPEDMAAQNPADQPRCRRRLGQRSS	180	
Qy	181	ROGSPGVSXKQPCDPLRLLLPPOFGVAITIGKEGATIRNTIKTQSKIDVHKENAGAA	240	
Db	181	ROGSPGVSXKQPCDPLRLLLPPOFGVAITIGKSGATIRNTIKTQSKIDVHKENAGAA	240	
Qy	241	EKSTITLITSTPEGTSAACKSILETMMKKEADQIKFTPEELPLKILANNHYGRLIGKGRULK	300	
Db	241	EKSTITLITSTPEGTSAACKSILETMMKKEADQIKFTPEELPLKILANNHYGRLIGKGRULK	300	
Qy	301	KIEDDPTKTTISPLQELIYLXNEERTIYKNVETCKAKKEEIMKIKREYENDIASNNL	360	
Db	301	KIEDDPTKTTISPLQELIYLXNEERTIYKNVETCKAKKEEIMKIKREYENDIASNNL	360	
Qy	361	QAHILIPGLNMLGLFPTSGMPRPPTSGPAMRPYPOFQOSESTERYHOFIPALSVGAI	420	
Db	361	QAHILIPGLNMLGLFPTSGMPRPPTSGPAMRPYPOFQOSESTERYHOFIPALSVGAI	420	
Qy	421	IGKGGHRIKQLSRFAGASIKRIATAEAPDAKRVNIITGPPEAFQAGRIYGIKEENFV	480	
Db	421	IGKGGHRIKQLSRFAGASIKRIATAEAPDAKRVNIITGPPEAFQAGRIYGIKEENFV	480	
Qy	481	SPKEEYVLEAHIRVSEFAAGVIGKGGKTVNELONLSSEAVVPRPDOTPEBNQVVVIT	540	
Db	481	SPKEEYVLEAHIRVSEFAAGVIGKGGKTVNELONLSSEAVVPRPDOTPEBNQVVVIT	540	

Oy 541 GHFYACOVAORAKIOEILITOVKHOQOQKALQSGPPOSRRK 579  
Db 541 GHFYACOVAORAKIOEILITOVKHOQOQKALQSGPPOSRRK 579

RESULT 4  
US-10-313-986-446  
; Sequence 446, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C19  
; CURRENT APPLICATION NUMBER: US/10/313,986  
; CURRENT FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 446  
; LENGTH: 579  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-313-986-446

Query Match 99.6%; Score 2943; DB 6; Length 579;  
Best Local Similarity 99.7%; Pred. No. 5.2e-243;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MNKLYIGNLSENNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGK 60  
Db 1 MNKLYIGNLSENNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGK 60  
Oy 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120  
Db 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120  
Oy 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Db 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Oy 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Db 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Oy 181 RQSGPVSVKOKPCDPLRLVLPFQVGAIIKGEATIRNITKQOSKIDVHRKENGAA 240  
Db 181 RQSGPVSVKOKPCDPLRLVLPFQVGAIIKGEATIRNITKQOSKIDVHRKENGAA 240  
Oy 241 EKSTIIISPEGTSACKSILEIMHKEADIKFTEIPLKILAHNPFVGRIGEGRNK 300  
Db 241 EKSTIIISPEGTSACKSILEIMHKEADIKFTEIPLKILAHNPFVGRIGEGRNK 300  
Oy 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Db 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Oy 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Db 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Oy 361 QAHILPGINNALGLPPTSGMPPTSGPSAMTPPYQFQESSE7YHOFIPALSGAI 420  
Db 361 QAHILPGINNALGLPPTSGMPPTSGPSAMTPPYQFQESSE7YHOFIPALSGAI 420  
Oy 421 IKGOGHIIKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Db 421 IKGOGHIIKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Oy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVVPVPRDQTPDENDDVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVVPVPRDQTPDENDDVVKIT 540  
Oy 541 GHFYACOVAORAKIOEILITOVKHOQOQKALQSGPPOSRRK 579  
Db 541 GHFYACOVAORAKIOEILITOVKHOQOQKALQSGPPOSRRK 579

RESULT 5

US-10-313-986-449  
; Sequence 449, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C19  
; CURRENT APPLICATION NUMBER: US/10/313,986  
; CURRENT FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 449  
; LENGTH: 579  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-313-986-449

Query Match 99.6%; Score 2943; DB 6; Length 579;  
Best Local Similarity 99.7%; Pred. No. 5.2e-243;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MNKLYIGNLSENNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGK 60  
Db 1 MNKLYIGNLSENNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGK 60  
Oy 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120  
Db 61 IELHGKPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120  
Oy 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Db 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Oy 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Db 121 VVNTYSSKQOAROLDKNGFLENFTLKVAIIPDEMAAQNPLQOPRGRRGIGOGSS 180  
Oy 181 RQSGPVSVKOKPCDPLRLVLPFQVGAIIKGEATIRNITKQOSKIDVHRKENGAA 240  
Db 181 RQSGPVSVKOKPCDPLRLVLPFQVGAIIKGEATIRNITKQOSKIDVHRKENGAA 240  
Oy 241 EKSTIIISPEGTSACKSILEIMHKEADIKFTEIPLKILAHNPFVGRIGEGRNK 300  
Db 241 EKSTIIISPEGTSACKSILEIMHKEADIKFTEIPLKILAHNPFVGRIGEGRNK 300  
Oy 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Db 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Oy 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Db 301 KIEDDTTKITISPLQELTYNPERTITVKGNETCANAEEIMKIRESEYENDIASMNL 360  
Oy 361 QAHILPGINNALGLPPTSGMPPTSGPSAMTPPYQFQESSE7YHOFIPALSGAI 420  
Db 361 QAHILPGINNALGLPPTSGMPPTSGPSAMTPPYQFQESSE7YHOFIPALSGAI 420  
Oy 421 IKGOGHIIKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Db 421 IKGOGHIIKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Oy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVVPVPRDQTPDENDDVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVVPVPRDQTPDENDDVVKIT 540  
Oy 541 GHFYACOVAORAKIOEILITOVKHOQOQKALQSGPPOSRRK 579  
Db 541 GHFYACOVAORAKIOEILITOVKHOQOQKALQSGPPOSRRK 579

RESULT 6  
US-10-313-986-480  
; Sequence 480, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro

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```
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-480

Query Match          99.6%; Score 2943; DB 6; Length 579;
Best Local Similarity 99.7%; Pred. No. 5.2e-243;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKALSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKALSGK 60
QY 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
DB 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
QY 121 VVNVYSSKDQARQALDKLNGFQLENFTLKVA3IPDEMAAQNPLQOPGRGRLGGRSS 180
DB 121 VVNVYSSKDQARQALDKLNGFQLENFTLKVA3IPDEMAAQNPLQOPGRGRLGGRSS 180
QY 181 RQSGPSVSKQPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
DB 181 RQSGPSVSKQPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
QY 241 EKSITILSTPREGTSAACKSILEIMHKEADIKFTEEIPKILAHNFVGRILGKGRNML 300
DB 241 EKSITILSTPREGTSAACKSILEIMHKEADIKFTEEIPKILAHNFVGRILGKGRNML 300
QY 301 KIEQDTDKRITISPLQELTYNPERTIVKGNVETCAKAEETIMKKIRRESYENDIASNML 360
DB 301 KIEQDTDKRITISPLQELTYNPERTIVKGNVETCAKAEETIMKKIRRESYENDIASNML 360
QY 361 QAHILPGLNMLNALGLPPTSGMPPTSGPSPAMTPPYPOFQOSETETVHOFIPALSVGAI 420
DB 361 QAHILPGLNMLNALGLPPTSGMPPTSGPSPAMTPPYPOFQOSETETVHOFIPALSVGAI 420
QY 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFGKOGRIYGIKEENFV 480
DB 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFGKOGRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
QY 541 GHFYACQVAQRKIOELITQVKHQOQKALQSGPPQSRK 579
DB 541 GHFYACQVAQRKIOELITQVKHQOQKALQSGPPQSRK 579

RESULT 7
US-10-313-986-486
; Sequence 486, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 586
; TYPE: PRT
```

```
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 486
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-486

Query Match          99.6%; Score 2943; DB 6; Length 589;
Best Local Similarity 99.7%; Pred. No. 5.3e-243;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKALSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKALSGK 60
QY 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
DB 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
QY 121 VVNVYSSKDQARQALDKLNGFQLENFTLKVA3IPDEMAAQNPLQOPGRGRLGGRSS 180
DB 121 VVNVYSSKDQARQALDKLNGFQLENFTLKVA3IPDEMAAQNPLQOPGRGRLGGRSS 180
QY 181 RQSGPSVSKQPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
DB 181 RQSGPSVSKQPCDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
QY 241 EKSITILSTPREGTSAACKSILEIMHKEADIKFTEEIPKILAHNFVGRILGKGRNML 300
DB 241 EKSITILSTPREGTSAACKSILEIMHKEADIKFTEEIPKILAHNFVGRILGKGRNML 300
QY 301 KIEQDTDKRITISPLQELTYNPERTIVKGNVETCAKAEETIMKKIRRESYENDIASNML 360
DB 301 KIEQDTDKRITISPLQELTYNPERTIVKGNVETCAKAEETIMKKIRRESYENDIASNML 360
QY 361 QAHILPGLNMLNALGLPPTSGMPPTSGPSPAMTPPYPOFQOSETETVHOFIPALSVGAI 420
DB 361 QAHILPGLNMLNALGLPPTSGMPPTSGPSPAMTPPYPOFQOSETETVHOFIPALSVGAI 420
QY 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFGKOGRIYGIKEENFV 480
DB 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFGKOGRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
QY 541 GHFYACQVAQRKIOELITQVKHQOQKALQSGPPQSRK 579
DB 541 GHFYACQVAQRKIOELITQVKHQOQKALQSGPPQSRK 579

RESULT 8
US-10-313-986-427
; Sequence 427, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
```

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; ORGANISM: Homo sapiens
US-10-313-986-427

Query Match          99.4%; Score 2937; DB 6; Length 586;
Best Local Similarity 99.7%; Pred. No. 1.4e-242;
Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKLTYGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSEWALKAIEALSCKI 61
    |||||||
DB 9 NKLTYGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSEWALKAIEALSCKI 68
    |||||||
QY 62 ELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYLDLSLVQYGVESCEQVNTDSETA 121
    |||||||
DB 69 ELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYLDLSLVQYGVESCEQVNTDSETA 128
    |||||||
QY 122 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGGRSS 181
    |||||||
DB 129 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGGRSS 188
    |||||||
QY 182 QSPGSGVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNITQOTSKIDVHRKENAGAA 241
    |||||||
DB 189 QSPGSGVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNITQOTSKIDVHRKENAGAA 248
    |||||||
QY 242 KSITTLSTPEGSTAACKSILEIMHKEADIKFTEEIPLKILAHNNFVGRLLGEGRNLLK 301
    |||||||
DB 249 KSITTLSTPEGSTAACKSILEIMHKEADIKFTEEIPLKILAHNNFVGRLLGEGRNLLK 308
    |||||||
QY 302 IEODDTTKITISPLQELTYNPERITTVKGNVETCAKAEELMKIRSEYENDIASMNLQ 361
    |||||||
DB 309 IEODDTTKITISPLQELTYNPERITTVKGNVETCAKAEELMKIRSEYENDIASMNLQ 368
    |||||||
QY 362 AHLIGLNLNALGLPPTSGMPPTSGPSAMTPPYPOEJOSETETVHOFIPALSVGAI 421
    |||||||
DB 369 AHLIGLNLNALGLPPTSGMPPTSGPSAMTPPYPOEJOSETETVHOFIPALSVGAI 428
    |||||||
QY 422 GKQGHIKQLSRFAGASIKIAPAEAPDAKVRWVITGPPEAFKAQGRYIKIEENFV 481
    |||||||
DB 429 GKQGHIKQLSRFAGASIKIAPAEAPDAKVRWVITGPPEAFKAQGRYIKIEENFV 488
    |||||||
QY 482 PKEEVKLEAHIRVPSFAGRGVIGKGGKTYNELQNLSSAEVVPROTDENDQVVKITG 541
    |||||||
DB 489 PKEEVKLEAHIRVPSFAGRGVIGKGGKTYNELQNLSSAEVVPROTDENDQVVKITG 548
    |||||||
QY 542 HFYACQVAORAKIOELITQVKGHOQKALOSGPPQSRK 579
    |||||||
DB 549 HFYACQVAORAKIOELITQVKGHOQKALOSGPPQSRK 586
    |||||||

RESULT 9
US-10-313-986-484
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andrea
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 579
; TYPE: PRT
; ORGANISM: primate
US-10-313-986-484

Query Match          99.4%; Score 2937; DB 6; Length 579;
Best Local Similarity 99.3%; Pred. No. 1.7e-242;
Matches 575; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSEWALKAIEALSCK 60
    |||||||
DB 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPDSEWALKAIEALSCK 60
    |||||||
QY 61 TELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYLDLSLVQYGVESCEQVNTDSETA 120
    |||||||
DB 61 TELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYLDLSLVQYGVESCEQVNTDSETA 120
    |||||||
QY 121 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGGRSS 180
    |||||||
DB 121 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPGRGRLGGRSS 180
    |||||||
QY 181 ROSPGSGVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNITQOTSKIDVHRKENAGAA 240
    |||||||
DB 181 ROSPGSGVSKOKPCDPLRLVPTQFVGAIIGKEGATIRNITQOTSKIDVHRKENAGAA 240
    |||||||
QY 241 EKSTTLSTPEGSTAACKSILEIMHKEADIKFTEEIPLKILAHNNFVGRLLGEGRNLLK 300
    |||||||
DB 241 EKSTTLSTPEGSTAACKSILEIMHKEADIKFTEEIPLKILAHNNFVGRLLGEGRNLLK 300
    |||||||
QY 301 KIEODDTTKITISPLQELTYNPERITTVKGNVETCAKAEELMKIRSEYENDIASMNL 360
    |||||||
DB 301 KIEODDTTKITISPLQELTYNPERITTVKGNVETCAKAEELMKIRSEYENDIASMNL 360
    |||||||
QY 361 QAHILIGLNLNALGLPPTSGMPPTSGPSAMTPPYPOEJOSETETVHOFIPALSVGAI 420
    |||||||
DB 361 QAHILIGLNLNALGLPPTSGMPPTSGPSAMTPPYPOEJOSETETVHOFIPALSVGAI 420
    |||||||
QY 421 IGKQGHIKQLSRFAGASIKIAPAEAPDAKVRWVITGPPEAFKAQGRYIKIEENFV 480
    |||||||
DB 421 IGKQGHIKQLSRFAGASIKIAPAEAPDAKVRWVITGPPEAFKAQGRYIKIEENFV 480
    |||||||
QY 481 SPKEEVKLEAHIRVPSFAGRGVIGKGGKTYNELQNLSSAEVVPROTDENDQVVKIT 540
    |||||||
DB 481 SPKEEVKLEAHIRVPSFAGRGVIGKGGKTYNELQNLSSAEVVPROTDENDQVVKIT 540
    |||||||
QY 541 GHFYACQVAORAKIOELITQVKGHOQKALOSGPPQSRK 579
    |||||||
DB 541 GHFYACQVAORAKIOELITQVKGHOQKALOSGPPQSRK 579
    |||||||

RESULT 10
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match          95.6%; Score 2826; DB 5; Length 558;
Best Local Similarity 99.8%; Pred. No. 5e-233;
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Thu Apr 17 07:55:18 2003

us-09-897-778-176.rapn

Page 6

Db 121 VVNVYSSKDOAROLDKNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGGRSS 180  
Qy 181 ROGSPGVSOKPCDPLRLVLPTQFVGAIIIGKEGATIRNTKOTQKIDVHKENAGAA 240  
Db 181 ROGSPGVSOKPCDPLRLVLPTQFVGAIIIGKEGATIRNTKOTQKIDVHKENAGAA 240  
Qy 241 EKSTIILSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIAHNNVGRILGKEGRNLK 300  
Db 241 EKSTIILSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIAHNNVGRILGKEGRNLK 300  
Qy 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360  
Db 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360  
Qy 361 OAHILPGNLNMGLEFPPTSGMPPTSGPPSAMTPPYPOFQSEETEVHOFIPALSVGAI 420  
Db 361 OAHILPGNLNMGLEFPPTSGMPPTSGPPSAMTPPYPOFQSEETEVHOFIPALSVGAI 420  
Qy 421 IKGOGHIKOLSRFAGASIKIAPAPADAKYRMVITITGPEADQKAGRIIGKEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAPADAKYRMVITITGPEADQKAGRIIGKEENFV 480  
Qy 481 SPKEEYKLEAHIRVPSFAGAVIGKGTIVNELONISSAEVYVPRDQTPDENQVYVKIT 540  
Db 481 SPKEEYKLEAHIRVPSFAGAVIGKGTIVNELONISSAEVYVPRDQTPDENQVYVKIT 540  
Qy 541 GHFYACQVAOKRIQ 554  
Db 541 GHFYACQVAOKRIK 554

RESULT 11

US-09-724-676A-92918  
Sequence 92918 Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-724-676A-92918

Query Match 95.6%; Score 2826; DB 5; Length 558;  
Best Local Similarity 99.8%; Pred. No. 3e-233;  
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSEMAAPSDLESIFDKAKIPVSGPFLVKTGYAFVDCPDDESMAKAIETALS GK 60  
Db 1 MNKLYIGNLSEMAAPSDLESIFDKAKIPVSGPFLVKTGYAFVDCPDDESMAKAIETALS GK 60  
Qy 61 IELHGKPIEVESHVSKRORIRKLOIRNIPHLQMEVLDLSLVQYGVVSCQOVNTDSETA 120  
Db 61 IELHGKPIEVESHVSKRORIRKLOIRNIPHLQMEVLDLSLVQYGVVSCQOVNTDSETA 120  
Qy 121 VVNVYSSKDOAROLDKNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGGRSS 180  
Db 121 VVNVYSSKDOAROLDKNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGGRSS 180  
Qy 181 ROGSPGVSOKPCDPLRLVLPTQFVGAIIIGKEGATIRNTKOTQKIDVHKENAGAA 240  
Db 181 ROGSPGVSOKPCDPLRLVLPTQFVGAIIIGKEGATIRNTKOTQKIDVHKENAGAA 240  
Qy 241 EKSTIILSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIAHNNVGRILGKEGRNLK 300  
Db 241 EKSTIILSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIAHNNVGRILGKEGRNLK 300  
Qy 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360  
Db 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360

Db 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360  
Qy 361 OAHILPGNLNMGLEFPPTSGMPPTSGPPSAMTPPYPOFQSEETEVHOFIPALSVGAI 420  
Db 361 OAHILPGNLNMGLEFPPTSGMPPTSGPPSAMTPPYPOFQSEETEVHOFIPALSVGAI 420  
Qy 421 IKGOGHIKOLSRFAGASIKIAPAPADAKYRMVITITGPEADQKAGRIIGKEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAPADAKYRMVITITGPEADQKAGRIIGKEENFV 480  
Qy 481 SPKEEYKLEAHIRVPSFAGAVIGKGTIVNELONISSAEVYVPRDQTPDENQVYVKIT 540  
Db 481 SPKEEYKLEAHIRVPSFAGAVIGKGTIVNELONISSAEVYVPRDQTPDENQVYVKIT 540  
Qy 541 GHFYACQVAOKRIQ 554  
Db 541 GHFYACQVAOKRIK 554

RESULT 12

US-09-724-676-92916  
Sequence 92916 Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-724-676-92916

Query Match 83.2%; Score 2459.5; DB 5; Length 492;  
Best Local Similarity 85.0%; Pred. No. 9.4e-202;  
Matches 492; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

Qy 1 MNKLYIGNLSEMAAPSDLESIFDKAKIPVSGPFLVKTGYAFVDCPDDESMAKAIETALS GK 60  
Db 1 MNKLYIGNLSEMAAPSDLESIFDKAKIPVSGPFLVKTGYAFVDCPDDESMAKAIETALS GK 60  
Qy 61 IELHGKPIEVESHVSKRORIRKLOIRNIPHLQMEVLDLSLVQYGVVSCQOVNTDSETA 120  
Db 61 IELHGKPIEVESHVSKRORIRKLOIRNIPHLQMEVLDLSLVQYGVVSCQOVNTDSETA 120  
Qy 121 VVNVYSSKDOAROLDKNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGGRSS 180  
Db 121 VVNVYSSKDOAROLDKNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGGRSS 180  
Qy 181 ROGSPGVSOKPCDPLRLVLPTQFVGAIIIGKEGATIRNTKOTQKIDVHKENAGAA 240  
Db 181 ROGSPGVSOKPCDPLRLVLPTQFVGAIIIGKEGATIRNTKOTQKIDVHKENAGAA 240  
Qy 241 EKSTIILSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIAHNNVGRILGKEGRNLK 300  
Db 241 EKSTIILSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLIAHNNVGRILGKEGRNLK 300  
Qy 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360  
Db 301 KIEODDTKITTISPLOELTLYNPERTITVKGAVETCAKAEIEIMKKIRSEYENDIASMNL 360  
Qy 361 OAHILPGNLNMGLEFPPTSGMPPTSGPPSAMTPPYPOFQSEETEVHOFIPALSVGAI 420  
Db 361 OAHILPGNLNMGLEFPPTSGMPPTSGPPSAMTPPYPOFQSEETEVHOFIPALSVGAI 420  
Qy 421 IKGOGHIKOLSRFAGASIKIAPAPADAKYRMVITITGPEADQKAGRIIGKEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAPADAKYRMVITITGPEADQKAGRIIGKEENFV 480

OY 481 SPKEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDENDQVVKIT 540  
Db 467 ----- 466  
OY 541 GHFYACQVAAQRKIOELITVOVKHOQAKALQSGPPQSRK 579  
Db 467 -----QELITVOVKHOQAKALQSGPPQSRK 492

## RESULT 13

US-09-724-676A-92916  
; Sequence 92916, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 92916  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-92916

Query Match 83.2%; Score 2459.5; DB 5; Length 492;  
Best Local Similarity 85.0%; Pred. No. 9,4e-202;  
Matches 492; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
OY 61 IELHGKPIEVESHVSPKRRIRKLOIRNIPHLQWEVLDLSLYQGVYVSCQEVNTDSETA 120  
Db 61 IELHGKPIEVESHVSPKRRIRKLOIRNIPHLQWEVLDLSLYQGVYVSCQEVNTDSETA 120  
OY 121 VVWVYSSKQARQALDLKNGFOLNFTLKAVYIPDEMAAQNPLOQPRGRGLGQSGSS 180  
Db 121 VVWVYSSKQARQALDLKNGFOLNFTLKAVYIPDEMAAQNPLOQPRGRGLGQSGSS 180  
OY 181 RQSGPSSVSKQPCDPLRLVPPQFVAGIIGKGAIRNITQOTQSKIDVHKENAGAA 240  
Db 181 RQSGPSSVSKQPCDPLRLVPPQFVAGIIGKGAIRNITQOTQSKIDVHKENAGAA 240  
OY 241 EKSITILSTPEGSTSAACKSILEIMHKEADIKFTEELPLKILAHNNFVGRLLGEGRNLK 300  
Db 241 EKSITILSTPEGSTSAACKSILEIMHKEADIKFTEELPLKILAHNNFVGRLLGEGRNLK 300  
OY 301 KTEODOTKITISPIQELITLYNPERTITVKNVETCAKAEELIMKIRRESEYENDIASMNL 360  
Db 301 KTEODOTKITISPIQELITLYNPERTITVKNVETCAKAEELIMKIRRESEYENDIASMNL 360  
OY 361 QAHLIPGLMLNGLFPTSGMPPTSGPSPAMTPPYPOFQESFETVHOFIPALSVGAI 420  
Db 361 QAHLIPGLMLNGLFPTSGMPPTSGPSPAMTPPYPOFQESFETVHOFIPALSVGAI 420  
OY 421 IKGQGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKAGRIYGIKENENV 480  
Db 421 IKGQGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKAGRIYGIKENENV 480  
OY 481 SPKEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDENDQVVKIT 540  
Db 467 ----- 466

OY 541 GHFYACQVAAQRKIOELITVOVKHOQAKALQSGPPQSRK 579  
Db 467 -----QELITVOVKHOQAKALQSGPPQSRK 492

RESULT 14  
US-10-313-986-500

; Sequence 500, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C19  
; CURRENT APPLICATION NUMBER: US/10/313,986  
; CURRENT FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 500  
; LENGTH: 577  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-313-986-500

Query Match 74.1%; Score 2191; DB 6; Length 577;  
Best Local Similarity 74.2%; Pred. No. 1.1e-178;  
Matches 435; Conservative 61; Mismatches 74; Indels 16; Gaps 8;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
OY 61 IELHGKPIEVESHVSPKRRIRKLOIRNIPHLQWEVLDLSLYQGVYVSCQEVNTDSETA 120  
Db 61 IELHGKPIEVESHVSPKRRIRKLOIRNIPHLQWEVLDLSLYQGVYVSCQEVNTDSETA 120  
OY 121 VVWVYSSKQARQALDLKNGFOLNFTLKAVYIPDEMAAQNPLOQPRGRGLGQSGSS 179  
Db 121 VVWVYSSKQARQALDLKNGFOLNFTLKAVYIPDEMAAQNPLOQPRGRGLGQSGSS 176  
OY 180 SROGSP---GSYSKQPCDPLRLVPPQFVAGIIGKGAIRNITQOTQSKIDVHKEN 236  
Db 177 PROGSFPAAGAPAKQOQVDPRLRLVPPQFVAGIIGKGAIRNITQOTQSKIDVHKEN 236  
OY 237 AGAERKSTILSTPEGSTSAACKSILEIMHKEADIKFTEELPLKILAHNNFVGRLLGEGRN 296  
Db 237 AGAERKSTILSTPEGSTSAACKSILEIMHKEADIKFTEELPLKILAHNNFVGRLLGEGRN 296  
OY 297 RNLKIBODOTKITISPIQELITLYNPERTITVKNVETCAKAEELIMKIRRESEYENDIA 356  
Db 297 RNLKIBODOTKITISPIQELITLYNPERTITVKNVETCAKAEELIMKIRRESEYENDIA 356  
OY 357 SMNLQAHLIPGLMLNGLFPTSGMPPTSGPSPAMTPPYPOFQESFETVHOFIP 413  
Db 357 AMSIQSHILPGLMLNGLFPTSGMPPTSGPSPAMTPPYPOFQESFETVHOFIP 413  
OY 414 ALSVAGIIGKQGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKAGRIYGI 473  
Db 414 AOVAVGALIGKQGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKAGRIYGI 473  
OY 474 IKENFVSPKEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDEND 533  
Db 474 LKEENFSPKEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDEND 533  
OY 534 QVWVYITGHFYACQVAAQRKIOELITVOVKHOQAKALQSGPPQSRK 579  
Db 534 QVWVYITGHFYACQVAAQRKIOELITVOVKHOQAKALQSGPPQSRK 577

RESULT 15  
US-09-724-676-48617  
; Sequence 48617, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676





GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:22:25 ; Search time 4.36783 Seconds  
(Without alignments)  
579,640 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 19  
Sequence: 1 TGYAFVDCPESMALKATE 19

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: /SID52/gcgdata/geneseq/geneseq_emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq_emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq_emb1/AA1983.DAT:*
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7: /SID52/gcgdata/geneseq/geneseq_emb1/AA1986.DAT:*
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20: /SID52/gcgdata/geneseq/geneseq_emb1/AA2000.DAT:*
21: /SID52/gcgdata/geneseq/geneseq_emb1/AA2001.DAT:*
22: /SID52/gcgdata/geneseq/geneseq_emb1/AA2002.DAT:*
23: /SID52/gcgdata/geneseq/geneseq_emb1/AA2003.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	19	100.0	579	21 AAB11328	Human lung cancer-
2	19	100.0	579	21 AAB11365	Human lung cancer
3	19	100.0	579	23 ABB74960	Human lung tumour
4	19	100.0	579	23 ABB74997	Human lung tumour
5	19	100.0	579	23 ABB75053	Human lung tumour
6	19	100.0	579	23 ABB75054	Human lung tumour
7	19	100.0	586	23 ABB75048	Human lung tumour
8	16	84.2	18	23 ABB75069	Human lung tumour
9	16	84.2	20	23 ABB75027	Human lung tumour
10	16	84.2	20	23 ABB75061	Human lung tumour

11	15	78.9	619	22 ABB21963	Novel human diagno
12	13	68.4	20	23 ABB75026	Human lung tumour
13	11	57.9	11	23 ABB75070	L533S antigenic ep
14	10	52.6	209	22 ABB71961	Novel human diagno
15	10	52.6	266	22 ABB12593	Novel human diagno
16	10	52.6	577	20 AAY30649	A murine c-myc cod
17	10	52.6	583	22 ABB12592	Novel human diagno
18	7	36.8	653	22 ABB67667	Drosophila melanog
19	6	31.6	10	23 AAM49781	Human KOC-associated
20	6	31.6	20	23 ABB75028	Human lung tumour
21	6	31.6	80	20 AAY22530	Drosophila sex-let
22	6	31.6	97	21 AAG03261	Human secreted pro
23	6	31.6	129	21 AAG04460	Arabidopsis thalia
24	6	31.6	147	23 ABB53886	Lactococcus lactis
25	6	31.6	157	18 AAM55589	H. pylori ORF 09CP
26	6	31.6	165	22 AAM59197	Propionibacterium
27	6	31.6	178	19 AAM98395	H. pylori GPO 86
28	6	31.6	178	19 AAM98262	T. thermophilus r1
29	6	31.6	180	22 AAM60391	Thermus thermophil
30	6	31.6	180	23 AAM48777	Thermus thermophil
31	6	31.6	180	23 AAM48778	Thermus thermophil
32	6	31.6	180	23 AAM48780	Thermus thermophil
33	6	31.6	180	23 AAM48781	Thermus thermophil
34	6	31.6	180	23 AAM48782	Thermus thermophil
35	6	31.6	180	23 AAM48783	Thermus thermophil
36	6	31.6	180	23 AAM48784	Thermus thermophil
37	6	31.6	180	23 AAM48785	Thermus thermophil
38	6	31.6	180	23 AAM48786	Thermus thermophil
39	6	31.6	180	23 AAM48787	Thermus thermophil
40	6	31.6	180	23 AAM48788	Thermus thermophil
41	6	31.6	180	23 AAM48789	Thermus thermophil
42	6	31.6	180	23 AAM48790	Thermus thermophil
43	6	31.6	180	23 AAM48791	Thermus thermophil
44	6	31.6	180	23 AAM48792	Thermus thermophil
45	6	31.6	185	18 AAM55195	H. pylori ORF 01ce

#### ALIGNMENTS

```

RESULT 1
ID AAB11328 standard: Protein: 579 AA.
AC AAB11328:
DT 21-FEB-2001 (first entry)
DE Human lung cancer-associated protein I5235.
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytosolic;
   vaccine; detection.
XX Homo sapiens.
XX OS
XX ID
XX PN WO20061612-A2.
XX PD 19-OCT-2000.
XX PF 03-APR-2000; 2000MO-US08896.
XX PR 02-APR-1999; 99US-0285479.
XX PR 17-DEC-1999; 99US-0466396.
XX PR 30-DEC-1999; 99US-0476496.
XX PR 10-JAN-2000; 2000US-0480884.
XX PR 22-FEB-2000; 2000US-0510376.
XX PA (CORI-) CORIXA CORP.
XX Wang T, Fan L.
XX WPI: 2000-628399/60.
XX N-PSDB: AAC65900.

```

```
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
XX Claim 3: Page 186-188; 261pp; English.
XX
XX This invention describes a novel isolated polypeptide (1) which
XX comprises an immunogenic portion of a lung tumor protein or variant (p2)
XX which has cytostatic activity and is used to inhibit the development of
XX cancer. Polynucleotides encoding the polypeptide (1) and the
XX polynucleotides are used in compositions and vaccines to inhibit the
XX development of cancer.
XX
XX especially lung cancer, in a patient. Methods described in the invention
XX can be used to monitor the progression of a cancer by carrying out the
XX detection at subsequent time points and comparing the results from the
XX different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
XX are treated with p2, polynucleotides encoding p2 or antigen presenting
XX cells expressing p2 and then administered to the patient to inhibit
XX development of cancer.
XX
XX Sequence 579 AA:
SQ
Query Match 100.0%; Score 19; DB 21; Length 579;
Best Local Similarity 100.0%; Pred. No. 2 1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGYAFVDCPDESMALKATE 19
DB 37 TGYAFVDCPDESMALKATE 55
RESULT 2
AB11365
ID AB11365 standard; Protein; 579 AA.
XX
XX AB11365:
XX
XX 21-FEB-2001 (first entry)
XX
XX Human lung cancer associated antigen L5235.
XX
XX Lung cancer; therapy: treatment; human; tumor; immunogenic; cytostatic;
XX vaccine; detection.
XX
XX Homo sapiens.
XX
XX MO200061612-AZ.
XX
XX 19-OCT-2000.
XX
XX 03-APR-2000; 2000MO-US08896.
XX
XX 02-APR-1999; 99US-0285479.
XX
XX 17-DEC-1999; 99US-0466396.
XX
XX 30-DEC-1999; 99US-0476496.
XX
XX 10-JAN-2000; 2000US-0480884.
XX
XX 22-FEB-2000; 2000US-0510376.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Fan L;
XX
XX WPI: 2000-628399/60.
XX
XX N-PSDB; AAC66035.
XX
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
XX Claim 3: Page 259-261; 261pp; English.
XX
XX This invention describes a novel isolated polypeptide (1) which
XX comprises an immunogenic portion of a lung tumor protein or variant (p2)
XX which have cytostatic activity. The polypeptides and polynucleotides are
```

```
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with p2, polynucleotides encoding p2 or antigen presenting
CC cells expressing p2 and then administered to the patient to inhibit
CC development of cancer.
CC
XX Sequence 579 AA:
SQ
Query Match 100.0%; Score 19; DB 21; Length 579;
Best Local Similarity 100.0%; Pred. No. 2 1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGYAFVDCPDESMALKATE 19
DB 37 TGYAFVDCPDESMALKATE 55
RESULT 3
AB174960
ID AB174960 standard; Protein; 579 AA.
XX
XX AB174960:
XX
XX 01-MAY-2002 (first entry)
XX
XX Human lung tumour L5235 protein sequence SEQ ID NO:176.
XX
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX immune response.
XX
XX Homo sapiens.
XX
XX WO200200174-A2.
XX
XX 03-JAN-2002.
XX
XX 28-JUN-2001; 2001WO-US21065.
XX
XX 28-JUN-2000; 2000US-0606421.
XX
XX 22-AUG-2000; 2000US-0613490.
XX
XX 21-AUG-2000; 2000US-0613490.
XX
XX 15-SEP-2000; 2000US-0662786.
XX
XX 09-OCT-2000; 2000US-0685696.
XX
XX 12-DEC-2000; 2000US-0735705.
XX
XX 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skelky YAM, Li SX, Kalos MD, Henderson RA;
XX McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
XX Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
XX
XX N-PSDB; ABL49119.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Example 2: Page 267-268; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
XX tumour proteins and polynucleotides have cytostatic and immunostimulant
XX activities, and can be used in vaccine production. Compositions
XX comprising the lung tumour proteins, polynucleotides, antibodies,
XX fusion proteins, T cell populations, or antigen presenting cells that
XX express the lung tumour proteins are useful for treating lung cancer or
XX stimulating an immune response. ABL48959 to ABL49300 and AB174946 to
XX AB175070 represent sequences used in the exemplification of the present
XX invention.
```

SQ Sequence 579 AA;

Query Match 100.0%; Score 19; DB 23; Length 579;

Best Local Similarity 100.0%; Pred. No. 2,1e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKATE 19  
|||||

DB 37 TGYAFVDCPDESMALKATE 55

RESULT 4

ABR74997

ID ABR74997 standard; Protein: 579 AA.

XX ABR74997;

AC ABR74997;

XX 01-MAY-2002 (first entry)

DT 01-MAY-2002 (first entry)

XX Human lung tumour L5235 protein sequence SEQ ID NO:348.

DE Human lung tumour L5235 protein sequence SEQ ID NO:348.

XX Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KM Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX Immune response.

OS Homo sapiens.

XX WO200200174-A2.

PN WO200200174-A2.

XX 03-JAN-2002.

PD 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0633597.

PR 13-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

PA (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McKenill PD, Fanger N, Rietter MW, Marneakis M, Fanger GR;

PI Vedick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI: 2002-090513/12.

DR N-PSDB; ABL49254.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Example 2; Page 330-332; 374pp; English.

PS The present invention describes human lung tumour proteins. Human lung

XX tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to

CC ABR75070 represent sequences used in the exemplification of the present

CC invention.

XX Sequence 579 AA;

SQ Sequence 579 AA;

Query Match 100.0%; Score 19; DB 23; Length 579;

Best Local Similarity 100.0%; Pred. No. 2,1e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKATE 19

DB 37 TGYAFVDCPDESMALKATE 55

RESULT 5  
ABR75053  
ID ABR75053 standard; Protein: 579 AA.

XX ABR75053;

AC ABR75053;

XX 01-MAY-2002 (first entry)

DT 01-MAY-2002 (first entry)

XX Human lung tumour L5235 recombinant protein sequence SEQ ID NO:446.

DE Human lung tumour L5235 recombinant protein sequence SEQ ID NO:446.

XX Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KM Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX Immune response.

OS Homo sapiens.

XX WO200200174-A2.

PN WO200200174-A2.

XX 03-JAN-2002.

PD 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0633597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

PA (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McKenill PD, Fanger N, Rietter MW, Marneakis M, Fanger GR;

PI Vedick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI: 2002-090513/12.

DR N-PSDB; ABL49254.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Claim 2; Page 365-367; 374pp; English.

PS The present invention describes human lung tumour proteins. Human lung

XX tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to

CC ABR75070 represent sequences used in the exemplification of the present

CC invention.

XX Sequence 579 AA;

SQ Sequence 579 AA;

Query Match 100.0%; Score 19; DB 23; Length 579;

Best Local Similarity 100.0%; Pred. No. 2,1e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKATE 19

DB 37 TGYAFVDCPDESMALKATE 55

RESULT 6  
ABR75054  
ID ABR75054 standard; Protein: 579 AA.

XX ABR75054;

AC ABR75054;

XX 01-MAY-2002 (first entry)

DT 01-MAY-2002 (first entry)

```

XX Human Lung tumour L523S recombinant protein sequence SEQ ID NO:449.
DE
XX Human: Lung tumour; Lung cancer; cytostatic; immunostimulant; vaccine;
KW Immune response.
XX
XX Homo sapiens.
OS
XX WO200200174-A2.
PN
XX 03-JAN-2002.
PD
XX
XX 28-JUN-2001; 2001WO-US21065.
PF
XX 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
DR N-PSDB; ABL49239.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response.
XX
XX Claim 2; Page 368-369; 374pp; English.
PS
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 579 AA;
SQ
XX
XX Query Match 100.0%; Score 19; DB 23; Length 579;
XX Best Local Similarity 100.0%; Pred. No. 2,1e-11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGYAFVDCPDSEWALKAIE 19
DB 37 TGYAFVDCPDSEWALKAIE 55

```

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XX 03-JAN-2002.
PD
XX 28-JUN-2001; 2001WO-US21065.
PF
XX 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
DR N-PSDB; ABL49283.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response.
XX
XX Claim 2; Page 354-355; 374pp; English.
PS
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 586 AA;
SQ
XX
XX Query Match 100.0%; Score 19; DB 23; Length 586;
XX Best Local Similarity 100.0%; Pred. No. 2,1e-11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGYAFVDCPDSEWALKAIE 19
DB 44 TGYAFVDCPDSEWALKAIE 62

```

XX WPI: 2002-090513/12.

PT Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

PS Claim 2; Page 348; 374pp: English.

XX The present invention describes human lung tumour proteins, human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions,

CC completing the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

CC ABB75070 represent sequences used in the exemplification of the present

CC invention.

XX Sequence 20 AA:

SQ

Query Match 84.2%; Score 16; DB 23; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.5e+09;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPDESMALKAE 19  
| | | | | | | | | | | | | | | | | | | | |  
DB 1 AFVDCPDESMALKAE 16

RESULT 10

ABB75061

ID ABB75061 standard; Peptide; 20 AA.

AC ABB75061:

XX 01-MAY-2002 (first entry)

DJ Human lung tumour L523S epitope SEQ ID NO:457.

DE Human lung tumour; lung cancer; cytosstatic; Immunostimulant; vaccine;

XX Human; lung tumour; lung cancer; cytosstatic; Immunostimulant; vaccine;

KW Immune response.

XX Homo sapiens.

O5 WO200200174-A2.

PN 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

PF 28-JUN-2001; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

PA Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;  
XX McNeill PD, Fanger N, Reiter MW, Manrarakis M, Fanger GR;  
PI Vedvick TS, Carter D, Matanabe Y, Peckham DM;  
PL WPI: 2002-090513/12.

DR Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Claim 2; Page 167; 374pp: English.

PS The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABl48959 to ABl49300 and ABB74946 to CC ABB75070 represent sequences used in the exemplification of the present invention.

XX Sequence 20 AA:  
SQ

Query Match 84.2%; Score 16; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 AFVDCPDSESMALKE 19  
DB 1 AFVDCPDSESMALKE 16

RESULT 11  
ABG21963  
ID ABG21963 standard; Protein; 619 AA.  
XX  
XX ABG21963;  
AC  
XX  
XX 18-FEB-2002 (first entry)  
DT  
XX  
XX Novel human diagnostic protein #21954.  
DE  
XX  
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200175067-A2.  
PN  
XX  
XX 11-OCT-2001.  
PD  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
PF  
XX  
XX 31-MAR-2000; 2000US-0540217.  
PR  
XX 23-AUG-2000; 2000US-0649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI: 2001-619362/73.  
DR  
XX N-PSDB: AAS86150.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
XX Claim 20; SEQ ID No 52322; 103pp; English.

The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to assist in identifying expressed genes. (I) is useful in gene therapy techniques  
XX to assist in identifying expressed genes. (I) is useful in gene therapy techniques  
XX (II) is useful for generating antibodies against it and for  
XX quantitating a polypeptide in tissue as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABB00010-ABG30377 represent novel human

diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO.  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

XX Sequence 619 AA:  
SQ

Query Match 78.9%; Score 15; DB 22; Length 619;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGAIFVDCPDSESMAL 15  
DB 73 TGAIFVDCPDSESMAL 87

RESULT 12  
ABB75026  
ID ABB75026 standard; Peptide; 20 AA.  
XX  
XX ABB75026;  
AC  
XX  
XX 01-MAY-2002 (first entry)  
DT  
XX  
XX Human lung tumour 15235 peptide SEQ ID NO:399.  
DE  
XX  
XX Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
KM immune response.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200200174-A2.  
PN  
XX  
XX 03-JAN-2002.  
PD  
XX  
XX 28-JUN-2001; 2001WO-US21065.  
PF  
XX  
XX 28-JUN-2000; 2000US-0606421.  
PR  
XX 02-AUG-2000; 2000US-0630940.  
XX 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
XX 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
XX 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang A, Svelky YAM, Li SX, Kalos MD, Henderson RA;  
XX McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
XX Vedvick TS, Carter D, Metanabe Y, Peckham DW;  
XX  
XX WPI: 2002-090513/12.  
DR  
XX  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
PT  
XX  
XX Claim 2; Page 348; 374pp; English.

The present invention describes human lung tumour proteins. Human lung  
XX tumour proteins and polynucleotides have cytostatic and immunostimulant  
XX activities, and can be used in vaccine production. Compositions  
XX comprising the lung tumour proteins, polynucleotides, antibodies,  
XX fusion proteins, T cell populations, polynucleotides, antibodies, that  
XX stimulate an immune response. ABl48959 to ABl49300 and ABB74946 to  
XX ABB75070 represent sequences used in the exemplification of the present  
XX invention.

XX Sequence 20 AA:  
SQ

Query Match 68.4%; Score 13; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAFVDCPDESM 13  
 |||||||  
 DB 8 TGAFVDCPDESM 20

## RESULT 13

ABR75070  
 ID ABR75070 standard; Peptide; 11 AA.

AC ABR75070;  
 XX

DT 01-MAY-2002 (first entry)  
 XX

DE L5235 antigenic epitope SEQ ID NO:466.  
 XX

KM Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
 XX immune response.  
 XX

OS Homo sapiens.  
 XX

PA W0200200174-A2.  
 XX

PD 03-JAN-2002.  
 XX

PF 28-JUN-2001; 2001MO-US21065.  
 XX

PR 28-JUN-2001; 2000US-0606421.  
 XX

PR 02-AUG-2000; 2000US-0630940.  
 XX

PR 21-AUG-2000; 2000US-0643397.  
 XX

PR 15-SEP-2000; 2000US-0662786.  
 XX

PR 09-OCT-2000; 2000US-0685696.  
 XX

PR 12-DEC-2000; 2000US-0735705.  
 XX

PR 07-MAY-2001; 2001US-0850716.  
 XX

XX (CORI-) CORIXA CORP.  
 XX

XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;  
 XX McNeill PD, Fanger N, Rietter MW, Marnerakis M, Fanger GR;  
 XX Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
 XX

XX WPI; 2002-090513/12.  
 XX

XX DR N-PSDB; ABL49300.  
 XX

XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
 XX lung cancer or stimulating an immune response -  
 XX

XX Claim 2; Page 168; 374pp; English.  
 XX

XX The present invention describes human lung tumour proteins. Human lung  
 XX tumour proteins and polynucleotides have cytostatic and immunostimulant  
 XX activities, and can be used in vaccine production. Compositions  
 XX comprising the lung tumour proteins, polynucleotides, antibodies,  
 XX fusion proteins, T cell populations, or antigen presenting cells that  
 XX express the lung tumour proteins are useful for treating lung cancer or  
 XX stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to  
 XX ABR75070 represent sequences used in the exemplification of the present  
 XX invention.  
 XX

XX Sequence 11 AA;  
 XX

XX Query Match 57.9%; Score 11; DB 23; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVDCPDESMAL 15  
 |||||||  
 DB 1 FVDCPDESMAL 11

RESULT 14  
 ABR21961  
 ID ABR21961 standard; Protein; 209 AA.

XX ABR21961;  
 XX 18-FEB-2002 (first entry)  
 XX

XX Novel human diagnostic protein #21952.  
 XX

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX food supplement; medical imaging; diagnostic; genetic disorder.  
 XX

XX Homo sapiens.  
 XX

XX W0200175067-A2.  
 XX

XX 11-OCT-2001.  
 XX

XX 30-MAR-2001; 2001MO-US08631.  
 XX

XX 31-MAR-2000; 2000US-0540217.  
 XX

XX 23-AUG-2000; 2000US-0649167.  
 XX

XX (HYSE-) HYSBO INC.  
 XX

XX Drmanac RT, Liu C, Tang YT;  
 XX

XX WPI; 2001-639362/73.  
 XX

XX DR N-PSDB; AAS86148.  
 XX

XX New isolated polynucleotide and encoded polypeptides, useful in  
 XX diagnostics, forensics, gene mapping, identification of mutations  
 XX responsible for genetic disorders or other traits and to assess  
 XX biodiversity -  
 XX

XX Claim 20; SEQ ID NO 52320; 103pp; English.  
 XX

XX The invention relates to isolated polynucleotide (I) and  
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 XX and gene mapping, and in recombinant production of (II). The  
 XX polynucleotides are also used in diagnostics as expressed sequence tags  
 XX for identifying expressed genes. (I) is useful in gene therapy techniques  
 XX to restore normal activity of (II) or to treat disease states involving  
 XX (II). (II) is useful for generating antibodies against it, detecting or  
 XX quantitating a polypeptide in tissue, as molecular weight markers and as  
 XX a food supplement. (II) and its binding partners are useful in medical  
 XX imaging of sites expressing (II). (I) and (II) are useful for treating  
 XX disorders involving aberrant protein expression or biological activity.  
 XX The polypeptide and polynucleotide sequences have applications in  
 XX diagnostics, forensics, gene mapping, identification of mutations in  
 XX responsible for genetic disorders or other traits to assess biodiversity  
 XX and to produce other types of data and products dependent on DNA and  
 XX amino acid sequences. ABR0010-ABG30377 represent novel human  
 XX diagnostic amino acid sequences of the invention.  
 XX Note: The sequence data for this patent did not appear in the printed  
 XX specification, but was obtained in electronic format directly from WIPO  
 XX at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

XX Sequence 209 AA;  
 XX

XX Query Match 52.6%; Score 10; DB 22; Length 209;  
 XX Best Local Similarity 100.0%; Pred. No. 0.01;  
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVDCPDE 11  
 |||||||  
 DB 15 GYAFVDCPDE 24

RESULT 15  
 ABR12593  
 ID ABR12593 standard; Protein; 266 AA.  
 XX ABR12593;  
 AC

XX	PT	18-FEB-2002	(first entry)	
XX	DE		Novel human diagnostic protein #12584.	
XX	XX		Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	XX		food supplement; medical imaging; diagnostic; genetic disorder.	
KW	XX			
OS	XX		Homo sapiens.	
XX	XX		WO200175067-A2.	
XX	XX		11-OCT-2001.	
XX	XX		30-MAR-2001, 2001WO-US08631.	
XX	XX		31-MAR-2000, 2000US-0540217.	
XX	XX		23-AUG-2000, 2000US-0649167.	
XX	XX		(HYSE-) HYSEQ INC.	
XX	XX		Drmancac RT, Liu C, Tang YF;	
XX	XX		WPI: 2001-639362/73.	
XX	XX		N-PSDB; AAS76/80.	
XX	XX		New isolated polynucleotide and encoded polypeptides, useful in	
XX	XX		diagnostics, forensics, gene mapping, identification of mutations	
XX	XX		responsible for genetic disorders or other traits and to assess	
XX	XX		biodiversity	
XX	XX		Claim 20; SEQ ID NO 42952; 103pp; English.	
XX	XX		The invention relates to isolated polynucleotide (I) and	
XX	XX		polynucleotide (II) sequences. (I) is useful as hybridisation probes,	
XX	XX		polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
XX	XX		and gene mapping, and are used in recombinant production as expressed	
XX	XX		polynucleotides are also used in diagnostics as expressed sequence tags	
XX	XX		for identifying expressed genes. (II) is useful in gene therapy, involving	
XX	XX		the use of the polynucleotide (II) in gene therapy, involving	
XX	XX		(II) it is useful for generating antibodies against it, detecting or	
XX	XX		quantitating a polypeptide in tissue, as molecular weight markers and as	
XX	XX		a food supplement. (II) and its binding partners are useful in medical	
XX	XX		imaging of sites expressing (II). (I) and (II) are useful for treating	
XX	XX		disorders involving aberrant protein expression or biological activity.	
XX	XX		The polypeptide and polynucleotide sequences have applications in	
XX	XX		diagnostics, forensics, gene mapping, identification of mutations	
XX	XX		and to produce other types of data and products dependent on mutations	
XX	XX		and to produce other types of data and products dependent on DNA and	
XX	XX		amino acid sequences. ABO0010-AB030377 represent novel human	
XX	XX		polynucleotide sequences of the invention.	
XX	XX		Note: The sequence data for this patent did not appear in the printed	
XX	XX		specification, but was obtained in electronic format directly from WIPO	
XX	XX		at ftp.wipo.int/pub/published_pat_sequences.	
XX	XX		Sequence 266 Aa:	
XX	XX		Query Match 53.6% Score 10; DB 22; Length 266;	
XX	XX		Best Local Similarity 100.0%; Pred. No. 0.012;	
XX	XX		Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	XX		2 GRAFVDCPDE 11	
XX	XX			
XX	XX		18 GRAFVDCPDE 27	

Search completed: April 16, 2003, 16:34:36  
 Job time : 5.36782 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:32:15 ; Search time 1.34154 Seconds  
(without alignments)  
416.711 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 19

Sequence: 1 TGYAFVDCPDESMALKAIE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfill1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	579	US-09-643-597-176	Sequence 176, App
2	19	100.0	579	US-09-643-597-348	Sequence 348, App
3	10	52.6	577	US-09-261-855-2	Sequence 2, Appl
4	6	31.6	72	US-08-973-273-27	Sequence 27, Appl
5	6	31.6	80	US-07-881-075-10	Sequence 10, Appl
6	6	31.6	80	US-08-120-827-10	Sequence 10, Appl
7	6	31.6	80	US-08-478-675-10	Sequence 10, Appl
8	6	31.6	443	US-09-134-001C-3183	Sequence 3183, Ap
9	6	31.6	461	US-09-134-001C-3821	Sequence 3821, Ap
10	5	26.3	8	US-08-902-623-3	Sequence 3, Appl
11	5	26.3	44	US-08-580-031A-22	Sequence 22, Appl
12	5	26.3	44	US-08-580-031A-23	Sequence 23, Appl
13	5	26.3	48	US-09-227-357-241	Sequence 241, Appl
14	5	26.3	50	US-08-580-031A-32	Sequence 32, Appl
15	5	26.3	87	US-09-227-357-544	Sequence 544, App
16	5	26.3	103	US-09-308-388-1	Sequence 1, Appl
17	5	26.3	105	US-08-965-056-52	Sequence 52, Appl
18	5	26.3	105	US-08-965-056-54	Sequence 54, Appl
19	5	26.3	122	US-08-477-451-36	Sequence 36, Appl
20	5	26.3	139	US-09-570-921-57	Sequence 57, Appl
21	5	26.3	158	US-08-356-397-4	Sequence 4, Appl
22	5	26.3	158	US-08-850-119-4	Sequence 4, Appl
23	5	26.3	158	US-09-098-900-1	Sequence 1, Appl
24	5	26.3	158	US-09-098-900-3	Sequence 3, Appl
25	5	26.3	158	US-08-806-877-1	Sequence 1, Appl
26	5	26.3	158	US-08-806-877-3	Sequence 3, Appl
27	5	26.3	187	US-08-493-071-16	Sequence 16, Appl

28	5	26.3	188	US-08-933-750C-39	Sequence 39, Appl
29	5	26.3	188	US-09-234-613-39	Sequence 39, Appl
30	5	26.3	204	US-08-965-056-106	Sequence 106, App
31	5	26.3	232	US-08-173-510B-84	Sequence 84, Appl
32	5	26.3	232	US-08-458-218-82	Sequence 82, Appl
33	5	26.3	232	US-08-450-497-84	Sequence 84, Appl
34	5	26.3	236	US-08-493-071-15	Sequence 15, Appl
35	5	26.3	253	US-09-180-109A-35	Sequence 35, Appl
36	5	26.3	254	US-09-180-109A-31	Sequence 31, Appl
37	5	26.3	259	US-08-997-080-98	Sequence 98, Appl
38	5	26.3	259	US-08-997-362-98	Sequence 98, Appl
39	5	26.3	259	US-08-873-970-98	Sequence 98, Appl
40	5	26.3	259	US-09-095-855-98	Sequence 98, Appl
41	5	26.3	259	US-09-324-542-98	Sequence 98, Appl
42	5	26.3	259	US-09-205-426-98	Sequence 98, Appl
43	5	26.3	267	US-08-965-056-38	Sequence 38, Appl
44	5	26.3	269	US-08-965-056-21	Sequence 21, Appl
45	5	26.3	277	US-08-690-457-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-643-597-176  
Sequence 176, Application US/09643597  
Patent No. 6426072

GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ. ID NOS.: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ. ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-176

Query Match 100.0%; Score 19; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.9e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 37 TGYAFVDCPDESMALKAIE 55  
1 TGYAFVDCPDESMALKAIE 19  
|||||

RESULT 2  
US-09-643-597-348  
Sequence 348, Application US/09643597  
Patent No. 6426072

GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-348

Query Match 100.0%; Score 19; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.9e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAAVDCPDSEWALKATE 19  
|||||

Db 37 TGAAVDCPDSEWALKATE 55

## RESULT 3

US-09-261-855-2  
Sequence 2, Application US/09261855A  
Patent No. 625055  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261,855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-2

Query Match 52.6%; Score 10; DB 4; Length 577;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVDCPDE 11  
|||||

Db 38 GYAFVDCPDE 47

## RESULT 4

US-08-973-273-27  
Sequence 27, Application US/08973273  
Patent No. 6140085  
GENERAL INFORMATION:  
APPLICANT: Dean, Caroline  
APPLICANT: MacKnight, Richard C  
APPLICANT: Bancroft, Ian  
APPLICANT: Lister, Clare K  
TITLE OF INVENTION: Genetic Control of Flowering  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderve P.C.  
STREET: 1100 No. 6140085th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,273  
FILING DATE: 01-DEC-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01332  
FILING DATE: 03-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9511196.9  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-29  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4100  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 72 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-973-273-27

Query Match 31.6%; Score 6; DB 4; Length 72;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVD 7  
|||||

Db 51 GYAFVD 56

## RESULT 5

US-07-881-075-10  
Sequence 10, Application US/07881075  
Patent No. 544149  
GENERAL INFORMATION:  
APPLICANT: KEENE, JACK D.  
APPLICANT: KING, PETER H.  
APPLICANT: LEVINE, TODD  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE  
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF  
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,  
P.C.  
STREET: 1755 Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,075  
FILING DATE: 19920511  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 544149man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 714-154-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 821-4500  
TELEFAX: (703) 486-2347  
TELEX: 248855 OPAT UR

;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 80 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-07-881-075-10

Query Match 31.6%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVD 7  
|||||  
DB 42 GYAFVD 47

RESULT 6  
US-08-120-827-10  
Sequence 10, Application US/08120827  
Patent No. 5525495  
GENERAL INFORMATION:  
APPLICANT: KEENE, JACK D.  
APPLICANT: KING, PETER H.  
APPLICANT: LEVINE, TODD  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE  
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS  
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
STREET: 1755 Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/120,827  
FILING DATE: 15-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5525495man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 714-158-0 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)413-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-120-827-10

Query Match 31.6%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVD 7  
|||||  
DB 42 GYAFVD 47

RESULT 7  
US-08-478-675-10

;; Sequence 10, Application US/08478675  
;; Patent No. 5773246  
;; GENERAL INFORMATION:  
;; APPLICANT: KEENE, JACK D.  
;; APPLICANT: KING, PETER H.  
;; APPLICANT: LEVINE, TODD  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE  
;; TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS  
;; TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION  
;; NUMBER OF SEQUENCES: 101  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: P.C.  
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
;; CITY: Arlington  
;; STATE: Virginia  
;; COUNTRY: U.S.A.  
;; ZIP: 22202  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/478,675  
;; FILING DATE: 07-JUN-1996  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/120,827  
;; FILING DATE: 15-SEP-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Oblon, No. 5773246man F.  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 714-158-0 CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703)413-3000  
;; TELEFAX: (703)413-2220  
;; TELEX: 248855 OPAT UR  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 80 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-478-675-10

Query Match 31.6%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVD 7  
|||||  
DB 42 GYAFVD 47

RESULT 8  
US-09-134-001C-3183  
Sequence 3183, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3183  
LENGTH: 443

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Page 4

TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3183

Query Match 31.6%; Score 6; DB 4; Length 443;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ALKAITE 19  
|||||  
DB 258 ALKAITE 263

RESULT 9

US-09-134-001C-3821  
Sequence 3821, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3821  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3821

Query Match 31.6%; Score 6; DB 4; Length 461;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFV 6  
|||||  
DB 252 TGYAFV 257

RESULT 10

US-08-902-623-3  
Sequence 3, Application US/08902623  
Patent No. 5822545  
GENERAL INFORMATION:  
APPLICANT: MATTHEAKIS, LARRY C.  
TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY  
TITLE OF INVENTION: LIBRARIES  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,623  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/586,176  
FILING DATE: 17-JAN-1996

APPLICATION NUMBER: US 08/300,262  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/144,775  
FILING DATE: US 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/12206  
FILING DATE: US 25-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: DUNN, TRACY J.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 16528X-003230US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-902-623-3

Query Match 26.3%; Score 5; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFV 6  
|||||  
DB 2 GYAFV 6

RESULT 11

US-08-580-031A-22  
Sequence 22, Application US/08580031A  
Patent No. 6428977  
GENERAL INFORMATION:  
APPLICANT: Graff, Jonathan M.  
APPLICANT: Woolf, Tod M.  
APPLICANT: Jin, Ping  
TITLE OF INVENTION: The "signalin" Family of TcPb Signal  
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,031A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: ONV-019,01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)832-1000  
TELEFAX: (617)832-7000  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-580-031A-22

Query Match 26.3%; Score 5; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKAIE 19  
DB 27 LKAIE 31

RESULT 12  
US-08-580-031A-23  
Sequence 23, Application US/08580031A  
Patent No. 6428977  
GENERAL INFORMATION:  
APPLICANT: Graff, Jonathan M.  
APPLICANT: Woolf, Tod M.  
APPLICANT: Jin, Ping  
APPLICANT: Melton, Douglas A.  
TITLE OF INVENTION: The "Signalin" Family of TGF $\beta$  Signal  
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,031A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: ONV-019,01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)832-1000  
TELEFAX: (617)832-7000  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-031A-23

Query Match 26.3%; Score 5; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKAIE 19  
DB 27 LKAIE 31

RESULT 13  
US-09-227-357-241  
Sequence 241, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357

CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 241  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Homo sapiens

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Page 6

FEATURE:  
NAME/KEY: SITE  
LOCATION: (48)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-227-357-241

Query Match 26.3%; Score 5; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SMLK 16  
DB 6 SMLK 10

RESULT 14  
US-08-580-031A-32  
Sequence 32, Application US/08580031A  
Patent No. 6428977  
GENERAL INFORMATION:  
APPLICANT: Graff, Jonathan M.  
APPLICANT: Woolf, Tod M.  
APPLICANT: Jin, Ping  
APPLICANT: Melton, Douglas A.  
TITLE OF INVENTION: The "Signalin" Family of TGF $\beta$  Signal  
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley Hoag & Eliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,031A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: ONV-019.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)832-1000  
TELEFAX: (617)832-7000  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-580-031A-32

Query Match 26.3%; Score 5; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKAIE 19  
DB 33 LKAIE 37

RESULT 15  
US-09-227-357-544  
Sequence 544, Application US/09227357  
Patent No. 6542581

GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
EARLIER FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 544  
LENGTH: 87  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-227-357-544

Query Match 26.3%; Score 5; DB 4; length 87;  
Best Local Similarity 100.0%; Pred No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SWALK 16  
Db 46 SWALK 50

Search completed: April 16, 2003, 16:38:11  
Job time : 2.34154 secs





Thu Apr 17 07:55:18 2003

us-09-897-778-176\_copy\_37\_55.Oligo.rapb

Page 1

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:36:47 ; Search time 2.18391 Seconds

(without alignments)  
657.841 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Sequence: 1 TGYAFVDCPDSEWALKAIE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 7561385 residues

Word size : 0

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCF\_NEW\_PUB\_PEP:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB\_PEP:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB\_PEP:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/FC105\_PUBCOMB\_PEP:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB\_PEP:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PEP:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB\_PEP:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB\_PEP:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB\_PEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	579	10	US-09-735-705-176 Sequence 176, App
2	19	100.0	579	10	US-09-735-705-348 Sequence 348, App
3	19	100.0	579	10	US-09-850-716A-176 Sequence 176, App
4	19	100.0	579	10	US-09-850-716A-348 Sequence 348, App
5	19	100.0	579	10	US-09-897-778-176 Sequence 176, App
6	19	100.0	579	10	US-09-897-778-348 Sequence 348, App
7	19	100.0	579	10	US-09-897-778-446 Sequence 446, App
8	19	100.0	579	10	US-09-897-778-446 Sequence 446, App
9	19	100.0	586	10	US-09-850-716A-427 Sequence 427, App
10	19	100.0	586	10	US-09-897-778-427 Sequence 427, App
11	19	84.2	18	10	US-09-897-778-465 Sequence 465, App
12	19	84.2	20	10	US-09-735-705-400 Sequence 400, App
13	19	84.2	20	10	US-09-850-716A-400 Sequence 400, App
14	19	84.2	20	10	US-09-897-778-457 Sequence 457, App
15	19	84.2	20	10	US-09-897-778-457 Sequence 457, App
16	19	68.4	20	10	US-09-735-705-399 Sequence 399, App
17	19	68.4	20	10	US-09-850-716A-399 Sequence 399, App
18	19	68.4	20	10	US-09-897-778-399 Sequence 399, App
19	11	57.9	11	10	US-09-897-778-466 Sequence 466, App

20	10	52.6	577	10	US-09-873-637-2	Sequence 2, App1
21	6	31.6	20	10	US-09-735-705-401	Sequence 401, App
22	6	31.6	20	10	US-09-850-716A-401	Sequence 401, App
23	6	31.6	20	10	US-09-897-778-401	Sequence 401, App
24	6	31.6	178	10	US-09-895-913A-20	Sequence 20, App1
25	6	31.6	178	10	US-09-881-752A-124	Sequence 124, App
26	6	31.6	286	10	US-09-815-242-10309	Sequence 10309, A
27	6	31.6	287	10	US-09-815-242-13772	Sequence 13772, A
28	6	31.6	332	10	US-09-738-626-5678	Sequence 5678, App
29	6	31.6	433	10	US-09-815-242-5283	Sequence 5283, App
30	6	31.6	436	10	US-09-815-242-12600	Sequence 12600, A
31	6	31.6	436	10	US-09-815-242-12732	Sequence 12732, A
32	6	31.6	620	10	US-09-764-864-1116	Sequence 1116, App
33	5	26.3	10	9	US-09-880-748-2200	Sequence 2200, App
34	5	26.3	36	10	US-09-779-451-33	Sequence 33, App1
35	5	26.3	38	10	US-09-779-451-34	Sequence 34, App1
36	5	26.3	44	12	US-10-095-492-22	Sequence 22, App1
37	5	26.3	44	12	US-10-095-492-23	Sequence 23, App1
38	5	26.3	45	10	US-09-779-451-32	Sequence 32, App1
39	5	26.3	48	9	US-09-983-802-241	Sequence 241, App1
40	5	26.3	50	12	US-10-095-492-32	Sequence 32, App1
41	5	26.3	54	10	US-09-764-860-549	Sequence 549, App
42	5	26.3	57	10	US-09-864-761-42064	Sequence 42064, A
43	5	26.3	68	9	US-10-078-770-142	Sequence 142, App
44	5	26.3	71	10	US-09-864-761-37078	Sequence 37078, A
45	5	26.3	77	9	US-10-078-770-152	Sequence 152, App

#### ALIGNMENTS

RESULT 1

US-09-735-705-176

Sequence 176 Application US/09735705

Parent NO. US200205329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Ajlun

APPLICANT: Skeiky, Yasin A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FASTSQ for Windows Version 3.0

SEQ ID NO 176

LENGTH: 579

TYPE: PRT

ORGANISM: Homo sapiens

US-09-735-705-176

Query Match 100.0% Score 19; DB 10; Length 579;

Best Local Similarity 100.0% Pred. No. 9.5e-13;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAIE 19

DB 37 TGYAFVDCPDSEWALKAIE 55

RESULT 2

US-09-735-705-348

Sequence 348 Application US/09735705

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; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-735-705-348

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 3
US-09-850-716A-176
; Sequence 176, Application US/09850716A
; Patent No. US2002015139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 4
US-09-850-716A-348
; Sequence 348, Application US/09850716A
; Patent No. US2002015139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.

; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-850-716A-348

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 5
US-09-897-778-176
; Sequence 176, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vegdick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-897-778-176

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 6
US-09-897-778-348
; Sequence 348, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vegdick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDESMALKATIE 19
Db 37 TGTAFTDCPDESMALKATIE 55

RESULT 7
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDESMALKATIE 19
Db 37 TGTAFTDCPDESMALKATIE 55

RESULT 8
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDESMALKATIE 19
Db 37 TGTAFTDCPDESMALKATIE 55

RESULT 9
US-09-850-716A-427
; Sequence 427, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kaios, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-427

Query Match          100.0%; Score 19; DB 10; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDESMALKATIE 19
Db 44 TGTAFTDCPDESMALKATIE 62

RESULT 10
US-09-897-778-427
; Sequence 427, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
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LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-427

Query Match 100.0%; Score 19; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 9,6e-13;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKATE 19  
|||||  
DB 44 TGYAFVDCPDSEWALKATE 62

RESULT 11  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnetakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 465  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-465

Query Match 84.2%; Score 16; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7,8e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALK 16  
|||||  
DB 1 TGYAFVDCPDSEWALK 16

RESULT 12  
US-09-735-705-400  
Sequence 400, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Banour, Chaitanya S.  
APPLICANT: Hosken, Nancy R.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skelley, Jasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-400

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8,5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDSEWALKATE 19  
|||||  
DB 1 AFVDCPDSEWALKATE 16

RESULT 13  
US-09-850-716A-400  
Sequence 400, Application US/09850716A  
Patent No. US2002013139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8,5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDSEWALKATE 19  
|||||  
DB 1 AFVDCPDSEWALKATE 16

RESULT 14  
US-09-897-778-400  
Sequence 400, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnetakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-400

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDDESMAKAE 19  
|||||  
DB 1 AFVDCPDDESMAKAE 16

## RESULT 15

US-09-897-778-457  
; Sequence 457, Application US/09897778  
; Patent No. US20020147143A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-457

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDDESMAKAE 19  
|||||  
DB 1 AFVDCPDDESMAKAE 16

Search completed: April 16, 2003, 16:48:43  
Job time : 4.18391 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:34:47 : Search time 12.8851 Seconds

(without alignments)  
950.708 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Sequence: 1 TGVAFVDCPDESMAKAE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Pending Patents AA Main: \*  
1: /cgn2\_6/ptodata/1/paa/US06.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US07.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US09.COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US10.COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US10.COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US10.COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US10.COMB.pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	19	100.0	43	US-10-117-982-482	Sequence 482, App
2	19	100.0	579	PCT-US01-47576-176	Sequence 176, App
3	19	100.0	579	PCT-US01-47576-348	Sequence 348, App
4	19	100.0	579	PCT-US01-47576-446	Sequence 446, App
5	19	100.0	579	PCT-US01-47576-449	Sequence 449, App
6	19	100.0	579	US-09-466-396A-176	Sequence 176, App

7	19	100.0	579	US-09-476-496A-176	Sequence 176, App
8	19	100.0	579	US-09-480-884A-176	Sequence 176, App
9	19	100.0	579	US-09-510-376A-176	Sequence 176, App
10	19	100.0	579	US-09-542-615A-176	Sequence 176, App
11	19	100.0	579	US-09-542-615A-348	Sequence 348, App
12	19	100.0	579	US-09-606-421A-176	Sequence 176, App
13	19	100.0	579	US-09-606-421A-348	Sequence 348, App
14	19	100.0	579	US-09-606-421B-176	Sequence 176, App
15	19	100.0	579	US-09-606-421B-348	Sequence 348, App
16	19	100.0	579	US-09-630-940A-176	Sequence 176, App
17	19	100.0	579	US-09-630-940A-348	Sequence 348, App
18	19	100.0	579	US-09-630-940B-176	Sequence 176, App
19	19	100.0	579	US-09-630-940B-348	Sequence 348, App
20	19	100.0	579	US-09-662-788-176	Sequence 176, App
21	19	100.0	579	US-09-662-788-348	Sequence 348, App
22	19	100.0	579	US-09-685-696-176	Sequence 176, App
23	19	100.0	579	US-09-685-696-348	Sequence 348, App
24	19	100.0	579	US-09-735-705-176	Sequence 176, App
25	19	100.0	579	US-09-735-705-348	Sequence 348, App
26	19	100.0	579	US-09-791-537-49019	Sequence 49019, A
27	19	100.0	579	US-09-791-537-86130	Sequence 86130, A
28	19	100.0	579	US-09-850-716-176	Sequence 176, App
29	19	100.0	579	US-09-850-716-348	Sequence 348, App
30	19	100.0	579	US-09-850-716A-176	Sequence 176, App
31	19	100.0	579	US-09-850-716A-348	Sequence 348, App
32	19	100.0	579	US-09-897-778-176	Sequence 176, App
33	19	100.0	579	US-09-897-778-348	Sequence 348, App
34	19	100.0	579	US-09-897-778-446	Sequence 446, App
35	19	100.0	579	US-09-897-778-449	Sequence 449, App
36	19	100.0	579	US-10-007-700-176	Sequence 176, App
37	19	100.0	579	US-10-007-700-348	Sequence 348, App
38	19	100.0	579	US-10-007-700-446	Sequence 446, App
39	19	100.0	579	US-10-007-700-449	Sequence 449, App
40	19	100.0	579	US-10-117-982-176	Sequence 176, App
41	19	100.0	579	US-10-117-982-348	Sequence 348, App
42	19	100.0	579	US-10-117-982-446	Sequence 446, App
43	19	100.0	579	US-10-117-982-449	Sequence 449, App
44	19	100.0	579	US-10-117-982-480	Sequence 480, App
45	19	100.0	579	US-10-117-982-484	Sequence 484, App

# ALIGNMENTS

RESULT 1  
US-10-117-982-482  
Sequence 482, Application US/10117982  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: Fangner, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darlick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Mericle, Barbara  
APPLICANT: Spies, Gregory A.  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C18  
CURRENT APPLICATION NUMBER: US/10/117.982  
CURRENT FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 484  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 482  
LENGTH: 43  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-117-982-482  
Query Match 100.0%, Score 19, DB 25, Length 43;





```

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-449

```

```

Query Match          100.0%; Score 19; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 6
US-09-466-396A-176
; Sequence 176, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.45504
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-396A-176

```

```

Query Match          100.0%; Score 19; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 7
US-09-476-496A-176
; Sequence 176, Application US/09476496A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

```

```

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.45505
; CURRENT APPLICATION NUMBER: US/09/476,496A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-496A-176

```

```

Query Match          100.0%; Score 19; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 8
US-09-480-884A-176
; Sequence 176, Application US/09480884A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.45506
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-884A-176

```

```

Query Match          100.0%; Score 19; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 9
US-09-510-376A-176
; Sequence 176, Application US/09510376A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.45507
; CURRENT APPLICATION NUMBER: US/09/510,376A
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens

```

Thu Apr 17 07:55:18 2003

us-09-897-778-176\_copy\_37\_55.Oligo.ram

Page 4

US-09-510-376A-176

Query Match 100.0%; Score 19; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKAE 19  
DB 37 TGYAFVDCPDESMAKAE 55

RESULT 10

US-09-542-615A-176  
Sequence 176, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542,615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKAE 19  
DB 37 TGYAFVDCPDESMAKAE 55

RESULT 11

US-09-542-615A-348  
Sequence 348, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542,615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKAE 19  
DB 37 TGYAFVDCPDESMAKAE 55

US-09-606-421A-176  
Sequence 176, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skelky, Yasir A.W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-606-421A-176

Query Match 100.0%; Score 19; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKAE 19  
DB 37 TGYAFVDCPDESMAKAE 55

RESULT 12

US-09-606-421A-348  
Sequence 348, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skelky, Yasir A.W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKAE 19  
DB 37 TGYAFVDCPDESMAKAE 55

RESULT 14

Query Match	100.0%;	Score 19;	DB 20;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 3.3e-12;		
Matches 19; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```

RESULT 15
US-09-606-421B-348
: Sequence 348, Application US/09606421B
: GENERAL INFORMATION:

```

```

1 APPLICANT: Wang, Tongtong
2 APPLICANT: Fan, Liqun
3 APPLICANT: Kalos, Michael D.
4 APPLICANT: Bangur, Chaltanya S.
5 APPLICANT: Hosken, Nancy
6 APPLICANT: Fanger, Gary R.
7 APPLICANT: Li, Samuel X.
8 APPLICANT: Wang, Aijun
9 APPLICANT: Skeiky, Yasir A.W.
10 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
11 FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
12 FILE REFERENCE: 210121.455C9
13 CURRENT APPLICATION NUMBER: US/09/606,421B
14 CURRENT FILING DATE: 2000-06-28
15 NUMBER OF SEQ ID NOS: 358
16 SOFTWARE: FastSeq for Windows Version 3.0
17 SEQ ID NO: 348
18 LENGTH: 579
19 TYPE: prt
20 ORGANISM: Homo sapiens
21 OS-09-606-421B-348

```

```

Query Match: 100.0%; Score 19; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 3, 3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TGAATVDCPDSSWALKAIE 19 .
      |||||||||
      37 TGAATVDCPDSSWALKAIE 55 .

```

Search completed: April 16, 2003, 16:45:12  
Job time : 13.8851 secs

2

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:35:32 ; Search time 3.93103 Seconds  
(without alignments)  
753.673 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 19  
Sequence: 1 TGYAFVDCPDSEWALKAIE 19

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 705215 seqs, 155932251 residues

Word size : 0

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending Patents AA New: \*  
1: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	43	US-10-313-986-482	Sequence 482, App
2	19	100.0	134	US-09-724-676-92917	Sequence 92917, A
3	19	100.0	134	US-09-724-676A-92917	Sequence 92917, A
4	19	100.0	492	US-09-724-676-92916	Sequence 92916, A
5	19	100.0	492	US-09-724-676A-92916	Sequence 92916, A
6	19	100.0	558	US-09-724-676-92918	Sequence 92918, A
7	19	100.0	558	US-09-724-676A-92918	Sequence 92918, A
8	19	100.0	579	US-10-313-986-176	Sequence 176, App
9	19	100.0	579	US-10-313-986-348	Sequence 348, App
10	19	100.0	579	US-10-313-986-446	Sequence 446, App
11	19	100.0	579	US-10-313-986-449	Sequence 449, App
12	19	100.0	579	US-10-313-986-480	Sequence 480, App
13	19	100.0	579	US-10-313-986-484	Sequence 484, App
14	19	100.0	586	US-10-348-119-255	Sequence 255, App
15	19	100.0	586	US-10-313-986-427	Sequence 427, App
16	19	100.0	589	US-10-313-986-486	Sequence 486, App
17	19	100.0	18	US-10-313-986-465	Sequence 465, App
18	19	100.0	20	US-10-313-986-400	Sequence 400, App
19	19	100.0	20	US-10-313-986-457	Sequence 457, App
20	19	100.0	20	US-10-313-986-508	Sequence 508, App
21	19	100.0	20	US-10-313-986-399	Sequence 399, App
22	19	100.0	20	US-10-313-986-470	Sequence 470, App
23	19	100.0	20	US-10-313-986-507	Sequence 507, App
24	19	100.0	11	US-10-313-986-466	Sequence 466, App
25	19	100.0	572	US-09-724-676-48617	Sequence 48617, A
26	19	100.0	572	US-09-724-676-48618	Sequence 48618, A

27	10	52.6	572	5	US-09-724-676A-48617	Sequence 48617, A
28	10	52.6	572	5	US-09-724-676A-48618	Sequence 48618, A
29	10	52.6	577	6	US-10-313-986-500	Sequence 500, App
30	10	52.6	598	5	US-09-724-676-48616	Sequence 48616, A
31	10	52.6	598	5	US-09-724-676-48621	Sequence 48621, A
32	10	52.6	598	5	US-09-724-676A-48616	Sequence 48616, A
33	10	52.6	598	5	US-09-724-676A-48621	Sequence 48621, A
34	10	52.6	602	5	US-09-724-676-48619	Sequence 48619, A
35	10	52.6	602	5	US-09-724-676-48620	Sequence 48620, A
36	10	52.6	602	5	US-09-724-676A-48619	Sequence 48619, A
37	10	52.6	602	5	US-09-724-676A-48620	Sequence 48620, A
38	6	31.6	20	6	US-10-313-986-401	Sequence 401, App
39	6	31.6	20	6	US-10-313-986-509	Sequence 509, App
40	6	31.6	75	6	US-10-282-122A-51701	Sequence 51701, A
41	6	31.6	97	5	US-09-513-999C-7342	Sequence 7342, App
42	6	31.6	120	6	US-10-366-683-24880	Sequence 24880, A
43	6	31.6	124	6	US-10-369-493-15644	Sequence 15644, A
44	6	31.6	124	6	US-10-369-493-16019	Sequence 16019, A
45	6	31.6	153	6	US-10-389-566-765	Sequence 765, App

#### ALIGNMENTS

```
RESULT 1
US-10-313-986-482
; Sequence 482, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Malanabe, Yoshitiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313, 986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 482
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-482

Query Match      100.0%; Score 19; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.2e-16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGYAFVDCPDSEWALKAIE 19
Db      5 TGYAFVDCPDSEWALKAIE 23

RESULT 2
US-09-724-676-92917
; Sequence 92917, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92917

Query Match      100.0%; Score 19; DB 5; Length 134;
```

Thu Apr 17 07:55:18 2003

us-09-897-778-176\_copy-37\_55.Oligo.rapn

Page 2

Best Local Similarity 100.0%; Pred. No. 2,5e-15;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDDESMALKAIE 19  
|||||

Db 37 TGYAFVDCPDDESMALKAIE 55

RESULT 3

US-09-724-676A-92917  
; Sequence 92917, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92917

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676A-92917

Query Match

Best Local Similarity 100.0%; Score 19; DB 5; Length 134;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDDESMALKAIE 19  
|||||

Db 37 TGYAFVDCPDDESMALKAIE 55

RESULT 4

US-09-724-676-92916  
; Sequence 92916, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92916

; LENGTH: 492

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676-92916

Query Match

Best Local Similarity 100.0%; Score 19; DB 5; Length 492;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-92916

Query Match  
Best Local Similarity 100.0%; Score 19; DB 5; Length 492;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDDESMALKAIE 19  
|||||

Db 37 TGYAFVDCPDDESMALKAIE 55

RESULT 6

US-09-724-676-92918  
; Sequence 92918, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92918

; LENGTH: 558

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676-92918

Query Match

Best Local Similarity 100.0%; Score 19; DB 5; Length 558;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDDESMALKAIE 19  
|||||

Db 37 TGYAFVDCPDDESMALKAIE 55

RESULT 7

US-09-724-676A-92918  
; Sequence 92918, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92918

; LENGTH: 558

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676A-92918

Query Match

Best Local Similarity 100.0%; Score 19; DB 5; Length 558;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDDESMALKAIE 19  
|||||

Db 37 TGYAFVDCPDDESMALKAIE 55

RESULT 8

US-10-313-986-176  
; Sequence 176, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92916

; LENGTH: 492

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676A-92916

Query Match

Best Local Similarity 100.0%; Score 19; DB 5; Length 492;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDDESMALKAIE 19  
|||||

Db 37 TGYAFVDCPDDESMALKAIE 55

```
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

RESULT 9
Query Match          100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      1 TGYAFVDCPDDESMALKATE 19
        |||
        37 TGYAFVDCPDDESMALKATE 55

RESULT 9
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

Query Match          100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      1 TGYAFVDCPDDESMALKATE 19
        |||
        37 TGYAFVDCPDDESMALKATE 55

RESULT 10
US-10-313-986-446
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
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```
; ORGANISM: Homo sapiens
US-10-313-986-446

Query Match          100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      1 TGYAFVDCPDDESMALKATE 19
        |||
        37 TGYAFVDCPDDESMALKATE 55

RESULT 11
US-10-313-986-449
; Sequence 449, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-449

Query Match          100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      1 TGYAFVDCPDDESMALKATE 19
        |||
        37 TGYAFVDCPDDESMALKATE 55

RESULT 12
US-10-313-986-480
; Sequence 480, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-480

Query Match          100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      1 TGYAFVDCPDDESMALKATE 19
        |||
        37 TGYAFVDCPDDESMALKATE 55
```

```
RESULT 13
US-10-313-986-484
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 484
; LENGTH: 579
; TYPE: PRT
; ORGANISM: primate
US-10-313-986-484

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 579;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSESWALKATE 19
Db 37 TGYAFVDCPDSESWALKATE 55

RESULT 14
US-10-348-119-255
; Sequence 255, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348.119
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 255
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-119-255

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 579;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSESWALKATE 19
Db 37 TGYAFVDCPDSESWALKATE 55

RESULT 15
US-10-313-986-427
; Sequence 427, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
```

```
FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-427

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 586;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSESWALKATE 19
Db 44 TGYAFVDCPDSESWALKATE 62

Search completed: April 16, 2003, 16:47:25
Job time : 4.93103 secs
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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:31:34 ; Search time 1.21675 Seconds  
(without alignments)  
1501.176 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 19

Sequence: 1 TGYAFVDCPDSESNALKAIE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	36.8	310	2	744857
2	7	36.8	337	2	130601
3	7	36.8	404	2	R39097
4	6	31.6	75	2	G37116
5	6	31.6	147	2	H86696
6	6	31.6	156	2	H84251
7	6	31.6	178	2	E71915
8	6	31.6	178	2	B64599
9	6	31.6	188	2	R83842
10	6	31.6	222	2	T47768
11	6	31.6	234	2	A12709
12	6	31.6	234	2	B97492
13	6	31.6	257	2	D69877
14	6	31.6	264	2	H97700
15	6	31.6	286	2	H90525
16	6	31.6	286	2	F65104
17	6	31.6	286	2	C91132
18	6	31.6	286	2	F85977
19	6	31.6	287	2	AC0899
20	6	31.6	313	2	G84335
21	6	31.6	318	2	B36972
22	6	31.6	318	2	S33433
23	6	31.6	319	2	T26450
24	6	31.6	324	2	D81452
25	6	31.6	340	2	C55070
26	6	31.6	340	2	UJ0292
27	6	31.6	340	2	T14921
28	6	31.6	354	2	R71312
29	6	31.6	354	2	B31639

30	6	31.6	366	2	B39725	sex-lethal sex det
31	6	31.6	367	2	A83825	peptidoglycan acet
32	6	31.6	377	2	C69955	peptidoglycan acet
33	6	31.6	397	2	T27950	hypothetical prote
34	6	31.6	399	2	S75862	translation elonga
35	6	31.6	436	2	C89926	hypothetical prote
36	6	31.6	450	2	E71909	hypothetical prote
37	6	31.6	460	2	G84246	phosphomannomutase
38	6	31.6	586	2	AD2493	hypothetical prote
39	6	31.6	620	2	B64379	hypothetical prote
40	6	31.6	749	2	G97782	hypothetical prote
41	6	31.6	770	2	A12421	hypothetical prote
42	6	26.3	47	2	T37086	probable IS elemen
43	5	26.3	59	2	C72203	hypothetical prote
44	5	26.3	65	2	H95007	hypothetical prote
45	5	26.3	68	2	S60688	env protein - huma

#### ALIGNMENTS

RESULT 1  
T44857  
Probable hydroxylase d [imported] - Amycolatopsis orientalis (fragment)  
C:Species: Amycolatopsis orientalis  
C:Date: 21-Jan-2000 #sequence-revision 21-Jan-2000 #text-change 16-Feb-2001  
C:Accession: T44857  
R:Solenberg, P.J.; Matsushima, P.; Stack, D.R.; Wilkie, S.C.; Thompson, R.C.; Baltz, submitted to the EMBL Data Library, January 1997  
A:Description: Production of hybrid glycopeptide antibiotics in vitro and in strepto  
A:Reference number: 222861  
A:Accession: T44857  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-310 <SOL>  
A:Cross-references: EMBL:U84350; PIDN:AA849296.1  
A:Experimental source: strain C329.4  
C:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology  
F:146-282/Domain: cytochrome P450 homology <P45>

Query Match  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPD 10  
DB 298 AFVDCPD 304

RESULT 2  
T30601  
Cytochrome P450 hydroxylase homolog PCZA361.27 - Amycolatopsis orientalis (fragment)  
N:Alternate names: PCZA361.27  
C:Species: Amycolatopsis orientalis  
C:Date: 21-Jan-2000 #sequence-revision 21-Jan-2000 #text-change 16-Feb-2001  
C:Accession: T30601  
R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard Chem. Biol. 3, 155-162, 1998  
A:Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin  
A:Reference number: 218804  
A:Accession: T30601  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-337 <VAN>  
A:Cross-references: EMBL:AJ223998  
C:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology  
F:173-309/Domain: cytochrome P450 homology <P45>

Query Match  
Best Local Similarity 36.8%; Score 7; DB 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 325 AFVDCPD 331
|||||
RESULT 3
F59097
Hypothetical protein PX01-54 - Bacillus anthracis virulence plasmid PX01
C:Species: Bacillus anthracis
C>Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C:Accession: F59097
R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Kellm, P.; Koehler
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of PX01, the large Bacillus anthracis plasmid harbored
A:Reference number: A59091; MUID:99445483; PMID:10515943
A:Accession: F59097
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1404 <KOR>
A:Cross-references: GB:AE065404; NID:94894216; PIDN:AD33258.1; PID:94894270
A:Experimental source: strain Sterne
A:Note: similar to S-layer precursor, surface layer protein (814 aa) B. anthracis (P490)
C:Genetics:
A:Gene: PX01-54
A:Genome: plasmid

Query Match 36.8%; Score 7; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SWALKAI 18
DB 175 SWALKAI 181

RESULT 4
G97116
Probable nucleic acid binding protein, containing KH domain [Imported] - Clostridium ace
C:Species: Clostridium acetobutylicum
C>Date: 12-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 17-May-2002
C:Accession: G97116
R:Nozling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koppin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G97116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: GB:AE001437; PIDN:AK79722.1; PID:915024725; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1756
C:Superfamily: Bacillus conserved hypothetical protein y1qC

Query Match 31.6%; Score 6; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 VCPPE 11
DB 13 VCPPE 18

RESULT 5
H86696
Hypothetical protein yfha [Imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: H86696
R:Belcino, A.; Wincker, P.; Manger, S.; Jallion, O.; Mairme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86696
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <STO>
A:Cross-references: GB:AE005176; PID:912723466; PIDN:AAK04674.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yfha
C:Superfamily: Escherichia coli hypothetical 16.4k protein (trfE-meta intergenic r

Query Match 31.6%; Score 6; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAI 19
DB 47 ALKAI 52

RESULT 6
H84251
H84251-related protein E [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84251
R:Ng, W.V.; Kennedy, S.P.; Mahairs, G.G.; Benquist, B.; Pan, M.; Shukla, H.D.; Lask
J.; Leihawaser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; J
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84251
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <STO>
A:Cross-references: GB:AE004437; NID:910580512; PIDN:AMG19380.1; GSPDB:GN00138
C:Genetics:
A:Gene: fapE

Query Match 31.6%; Score 6; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAI 19
DB 97 ALKAI 102

RESULT 7
E71915
hydrogenase maturation factor hyad [Similarity] - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Sep-2000
C:Accession: E71915
R:Lim, R.A.; Ling, L.S.L.; Molt, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D
J.; Ives, C.; Gibson, R.; Werbey, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Voyis, G.F
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71915
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <ARN>
A:Cross-references: GB:AE001490; GB:AE001439; NID:94155115; PIDN:AD06149.1; PID:9415
A:Experimental source: strain J99
C:Genetics:
A:Gene: hyad
C:Superfamily: Escherichia coli hydrogenase-1 maturation factor hyad

Query Match 31.6%; Score 6; DB 2; Length 178;
```

Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ALKAIE 19  
|||||

Db 144 ALKAIE 149

#### RESULT 8

B64599

hydrogenase maturation factor HP0634 [similarity] - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C>Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 02-Sep-2000

C:Accession: B64599

R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodok, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; PMID:97394467; PMID:9252185

A:Accession: B64599

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-178 <TOM>

A:Cross-references: GB:AE000577; GB:AE000511; NID:92313747; PIDN:AA07694.1; PID:9231375

C:Superfamily: Escherichia coli hydrogenase-1 maturation factor hyad

#### Query Match

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ALKAIE 19  
|||||

Db 144 ALKAIE 149

#### RESULT 9

F83842

stage V sporulation protein AE spovAE [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C:Accession: F83842

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83842

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-188 <STO>

A:Cross-references: GB:AP001512; GB:BA000004; NID:910174030; PIDN:BA05261.1; GSPDB:GN00

C:Genetics:

A:Experimental source: strain C-125

C:Gene: spovAE

#### Query Match

Best Local Similarity 100.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ALKAIE 19  
|||||

Db 16 ALKAIE 21

#### RESULT 10

T47768

hypothetical protein F2413.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 19-May-2000

C:Accession: T47768

R:Nyakatura, G.; Fartmann, B.; Daner, D.; Sterr, W.; Holland, R.; Welchselgartner, M.;

submitted to the Protein Sequence Database, February 2000

A:Reference number: 224475

A:Accession: T47768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <NYA>

A:Cross-references: EMBL:AL138655

A:Experimental source: cultivar Columbia; BMC clone F2413

C:Genetics:

A:Map position: 3

A:Introns: 84/3; 143/3; 181/3

A>Note: F2413.160

C:Superfamily: DNA-directed RNA polymerase chain RPB5

#### Query Match

Best Local Similarity 100.0%; Pred. No. 25;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ALKAIE 19  
|||||

Db 128 ALKAIE 133

#### RESULT 11

A12709

branched-chain amino acid permease Atutl082 [imported] - Agrobacterium tumefaciens (st

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Mar-2002

C:Accession: A12709

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.F.; Chen, Y.; Woo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutylav, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: A12709

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KIR>

A:Cross-references: GB:AE008688; PIDN:AML42095.1; PID:917739477; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atutl082

A:Map position: circular chromosome

C:Superfamily: hypothetical protein b2682

#### Query Match

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DESNAL 15  
|||||

Db 113 DESNAL 118

#### RESULT 12

B97492

azic family protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 01-Mar-2002

C:Accession: B97492

R:Goodner, B.; Hinkle, G.; Gattling, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: B97492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE007869; PIDN:AKK86891.1; PID:915156113; GSPDB:GN00169

C:Genetics:

A:Gene: AGR\_C\_2001  
 A:Map position: circular chromosome  
 C:Superfamily: hypothetical protein b2682

Query Match 31.6%; Score 6; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DESMAL 15  
 DB 113 DESMAL 118

## RESULT 13

D69877 uroporphyrin-III C-methyltransferase homolog yind - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000

C:Accession: D69877

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertier, C.; Bron, S.; Brouillet, S.; Buschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choc, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaui, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Laubert, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogilwara, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Salto, T.M.; Portetlelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Salto, T.M.; Portetlelle, A:Authors: Schlach, S.; Schroeter, R.; Scorfone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Schlach, S.; Tanakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A:Reference number: A65580; MUID:98044033; PMID:9384377

A:Accession: D69877

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-257 <KUN>

A:Cross-references: GB:AL009112; GB:AL009126; NID:g2633902; PIDN:CAR13435.1; PID:g2633934

A:Experimental source: strain 168

C:Genetics:

A:Gene: yind

C:Superfamily: S-adenosyl-L-methionine uroporphyrinogen methyltransferase

Query Match 31.6%; Score 6; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19  
 DB 21 ALKAIE 26

## RESULT 14

H97700 hypothetical protein lpxa [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 22-Oct-2001

C:Accession: H97700

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A:Reference number: A97700; MUID:21442074; PMID:1157893

A:Accession: H97700

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-264 <KUR>

A:Cross-references: GB:AE006914; PIDN:AA102546.1; PID:g15619040; GSPDB:GN00173

C:Genetics:

A:Gene: lpxa

C:Superfamily: UDP-N-acetylglucosamine acyltransferase

Query Match 31.6%; Score 6; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19  
 DB 21 ALKAIE 26

## RESULT 15

F90525 fructose-bisphosphate aldolase [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001

C:Accession: F90525

R:Chambaud, I.; Heilbr, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: F90525

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <KUR>

A:Cross-references: GB:AL445566; PID:g14089523; PIDN:CAC13283.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPu\_1100

C:Superfamily: fructose-bisphosphate aldolase II

Query Match 31.6%; Score 6; DB 2; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19  
 DB 91 ALKAIE 96

Search completed: April 16, 2003, 16:37:39  
 Job time : 3.21675 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:23:10 ; Search time 0.967159 Seconds

(without alignments)  
814.809 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 19  
Sequence: 1 TGYAFVDCPDESWALKRAIE 19

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	31.6	75	YH56_CIOAB	097196 clostridium
2	6	31.6	185	RRE_THERH	09x776 thermus the
3	6	31.6	264	LPXA_RICCN	092199 rickettsia
4	6	31.6	264	LPXA_RICCN	P32199 rickettsia
5	6	31.6	286	YRAL_ECCLI	P45528 escherichia
6	6	31.6	307	SXL_CHRRU	097018 chrysomya r
7	6	31.6	318	SOLR_CIOAB	P33746 clostridium
8	6	31.6	324	FABH_CAMJE	09p1h1 campylobact
9	6	31.6	324	SXL_MUSDO	017310 musca domes
10	6	31.6	340	RECA_THERH	P48297 thermus the
11	6	31.6	348	SXL_CERCA	061374 ceratilis c
12	6	31.6	349	ISPG_CIOPE	P58667 clostridium
13	6	31.6	354	SXL_DROME	P19339 drosophila
14	6	31.6	354	SXL_DROSU	024688 drosophila
15	6	31.6	367	ISPG_BACHD	09k18 bacillus ha
16	6	31.6	377	ISPG_BACSD	P54482 bacillus su
17	6	31.6	399	EPNU_FERIS	050340 ferrisobact
18	6	31.6	399	EPNU_SYNY3	P74227 synecocyst
19	6	31.6	620	1634_MERUA	058051 methanococ
20	6	26.3	58	1E12_HSV2	P14345 herpes simp
21	5	26.3	88	RL37_CANAL	09p36 candida alb
22	5	26.3	92	RPOL_SULSO	0980K0 sulfolobus
23	5	26.3	96	RS20_THEMA	09x1Y7 thermotoga
24	5	26.3	101	RS14_CAUCR	09a8u0 caulobacter
25	5	26.3	101	RS14_RHITO	09a8u4 rhizobium l
26	5	26.3	107	HIS2_AGRIS	08u191 agrobacteri
27	5	26.3	112	Y13K_SSVI	P20220 sulfolobus
28	5	26.3	119	YBX4_YEAST	P38269 saccharomyc
29	5	26.3	129	PFD4_YEAST	P53900 saccharomyc
30	5	26.3	133	Y54L_SYNY3	P72777 synecocyst
31	5	26.3	144	SODM_EPRST	P28762 eptatretus
32	5	26.3	152	YUVS_BPPHV	P13004 lactococcus
33	5	26.3	157	ALS2_HUMAN	P56377 h adapter-r

34	5	26.3	158	1	ALS1_HUMAN	000382 h adapter-r
35	5	26.3	160	1	ALS2_MOUSE	09db50 m adapter-r
36	5	26.3	160	1	HPK_AQUAE	06550 aquifex aeo
37	5	26.3	160	1	HPK_HAETN	P43777 haemophilus
38	5	26.3	174	1	ARF6_XENIA	P51645 xenopus lae
39	5	26.3	181	1	YNEA_BACSU	P42408 bacillus su
40	5	26.3	185	1	SYN4_XENIA	009004 xenopus lae
41	5	26.3	186	1	FINO_ECO57	082922 escherichia
42	5	26.3	186	1	FINO_ECOLI	P22707 escherichia
43	5	26.3	186	1	FI02_ECOLI	P08315 escherichia
44	5	26.3	186	1	FI03_ECOLI	P29367 escherichia
45	5	26.3	186	1	FI04_ECOLI	005781 escherichia

## ALIGNMENTS

RESULT 1	YH56_CIOAB	STANDARD;	PRT;	75 AA.
ID	YH56_CIOAB			
AC	097196;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hypothetical protein CAC1756.			
GN	CAC1756.			
OS	Clostridium acetobutylicum.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_TaxID=1488;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ATCC 824 / DSM 792 / VKM B-1787;			
RX	MEDLINE=21359325; PubMed=1146286;			
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,			
RA	Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,			
RA	Tatunov R.L., Sabatle F., Doucette-Stamm L., Souaille P., Daly M.J.,			
RA	Bennett G.N., Koonin E.V., Smith D.R.;			
RT	"Genome sequence and comparative analysis of the solvent-producing			
RT	Bacterium Clostridium acetobutylicum.";			
RT	J. Bacteriol. 183:4823-4838(2001).			
RL	J. Bacteriol. 183:4823-4838(2001).			
CC	1- SIMILARITY: BELONGS TO THE UPF0109 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; AE007684; AAK79722.1;			
DR	PROSITE; PS50084; KH_TYPE.1; FALSE NEG.			
KW	Hypothetical protein; RNA-binding; Complete proteome.			
FT	DOMAIN 29			
SO	SEQUENCE 75 AA; 8170 MW; A68E213FAFEZDE CRC64;			
Query Match	31.6%; Score 6; DB 1; Length 75;			
Best Local Similarity	100.0%; Pred. No. 4.1;			
Matches	6; Conservative			
QY	6 VDCPDE 11			
DB	13 VDCPDE 18			
RESULT 2	RRE_THERH	STANDARD;	PRT;	185 AA.
ID	RRE_THERH			
AC	09x776;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			

```

DE Ribosome recycling factor (Ribosome releasing factor) (RRF).
GN RRF.
OS Thermus thermophilus.
CC Bacteria: Thermus/Delinooccus group; Delinococci; Thermates;
CC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9229778; PubMed-10214965;
RA Fujiwara T., Ito K., Nakayashiki T., Nakamura Y.;
RT "Number mutations in ribosome recycling factors of Escherichia coli and
RT Thermus thermophilus: evidence for C-terminal modulator element.";
RL FEBS Lett. 447:297-302(1999).
CC -1- FUNCTION: RESPONSIBLE FOR THE RELEASE OF RIBOSOMES FROM MESSENGER
CC RNA AT THE TERMINATION OF PROTEIN BIOSYNTHESIS. MAY INCREASE THE
CC EFFICIENCY OF TRANSLATION BY RECYCLING RIBOSOMES FROM ONE ROUND OF
CC TRANSLATION TO ANOTHER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (By similarity).
CC
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CC
DR EMBL: AB016498; BAA76865.1;
DR HSP: Q9X1B9; IDDS.
DR InterPro: IPR002861; RRF.
DR Pfam: PF01763; RRF; 1.
DR TIGRPFAM: TIGR00496; Irf; 1.
KM Protein biosynthesis.
SQ SEQUENCE 185 AA; 20994 MW; F3135AE7F813328 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19
Db 75 ALKAIE 80
|||||

RESULT 3
LPXA_RICCN STANDARD; PRT; 264 AA.
AC Q92309;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase
DE (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
GN LPXA OR PC0008.
OS Rickettsia conorii.
CC Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
CC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-Malish 7;
RX MEDLINE-21442074; PubMed-11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samon D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001)
CC -1- FUNCTION: Involved in the biosynthesis of lipid A, a
CC phosphorylated glycolipid that anchors the lipopolysaccharide to
CC the outer membrane of the cell (by similarity).
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
protein] + UDP-N-acetylglucosamine -> [acyl-carrier protein] +

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CC UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
CC -1- PATHWAY: Lipid A biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC
CC -1- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
CC LPXA SUBFAMILY
CC
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CC
DR EMBL: AE008569; AA02546.1;
DR InterPro: IPR01431; Hexapep-transf.
DR Pfam: PF00132; Hexapep; 7.
DR PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
KM Repeat: Complete proteome.
SQ SEQUENCE 264 AA; 28513 MW; 0BF3119FC85D624 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19
Db 213 ALKAIE 218
|||||

RESULT 4
LPXA_RICRI STANDARD; PRT; 264 AA.
AC P32199;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase
DE (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
GN LPXA.
OS Rickettsia rickettsii.
CC Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
CC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94171066; PubMed-8125326;
RX Shaw E.I., Wood D.O.;
RT "Characterization of a Rickettsia rickettsii DNA fragment analogous
RT to the fir A-ORF17-lpxA region of Escherichia coli.";
RL Gene 140:109-113(1994).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
CC PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOPOLYSACCHARIDE TO
CC THE OUTER MEMBRANE OF THE CELL.
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
protein] + UDP-N-acetylglucosamine -> [acyl-carrier protein] +
CC UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
CC -1- PATHWAY: Lipid A biosynthesis; first step.
CC -1- SUBUNIT: HOMOTRIMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
CC LPXA SUBFAMILY
CC
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DR EMBL: L22690; AAA26386.1; -  
 DR HSSP: P10440; 1LXA.  
 DR InterPro: IPR001451; Hexapep\_transf.  
 DR Pfam: PF00132; hexapep; 7  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERASS; 1.  
 DR Transferrase; Acyltransferase; Lipid A biosynthesis; Lipid synthesis;  
 KW Repeat.  
 SQ SEQUENCE 264 AA; 28333 MW; 7A24B38C76A596D0 CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 14 ALKALIE 19  
 Db 213 ALKALIE 218  
 RESULT 5  
 ID YRAL\_ECOLI STANDARD; PRT; 286 AA.  
 AC P45528;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yral.  
 GN YRAL OR B3146 OR Z4505 OR ECS4027.  
 OS Escherichia coli O157:H7.  
 OC Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562, 83334;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RA Balthier F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimmalanta E.T., Potamocis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Balthier F.R.;  
 RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:529-533(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=1125776;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Tida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kunara S., Shiba T., Hattori M., Shingawa M.;  
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22(2001).  
 CC -1 SIMILARITY: BELONGS TO THE UPF0011 FAMILY. STRONG, TO H.INFLUENZAE  
 CC H1654.  
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 CC -----  
 DR EMBL: U18997; AAA57949.1; -  
 DR EMBL: AE000395; AAC76180.1; -  
 DR EMBL: AE005543; AAG58282.1; -  
 DR EMBL: AP002564; BAB37450.1; -  
 DR EcoGene: EG12777; yral.  
 DR InterPro: IPR000878; Cor/por\_Mettransf.  
 DR InterPro: IPR000578; UPF0011.  
 DR Pfam: PF00590; TP\_methylase; 1.  
 DR TIGRFAMs: TIGR00096; UPF0011; 1.  
 DR PROSITE: PS01296; UPF0011; 1.  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 286 AA; 31348 MW; 886EA92858BP95C CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 14 ALKALIE 19  
 Db 155 ALKALIE 160  
 RESULT 6  
 ID SXL\_CHRRU STANDARD; PRT; 307 AA.  
 AC O97018;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sex-lethal protein homolog.  
 GN SXL.  
 OS Chrysomya rufifacies (Hairy maggot blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Oestroidea; Calliphoridae; Chrysomya.  
 OX NCBI\_TaxID=45450;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96029145; PubMed=7563134;  
 RA Mueller-Holtkamp F.;  
 RT "The Sex-lethal gene homologue in Chrysomya rufifacies is highly  
 RT conserved in sequence and exon-intron organization.";  
 RL J. Mol. Evol. 41:467-477(1995).  
 CC -1 FUNCTION: UNKNOWN. APPARENTLY NOT INVOLVED IN SOMATIC SEX  
 CC DETERMINATION.  
 CC -1 SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1 ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE PRODUCED BY  
 CC SEX-INDEPENDENT ALTERNATIVE SPLICING.  
 CC -1 DEVELOPMENTAL STAGE: EXPRESSED IN BOTH SEXES FROM THE ONSET OF THE  
 CC CELLULAR BLASTODERM FORMATION THROUGHOUT DEVELOPMENT.  
 CC -1 SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
 CC -1 CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.  
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 CC -----  
 DR EMBL: S79722; -; NOT\_ANNOTATED\_CDS.  
 DR HSSP: P19339; ISXL.  
 DR InterPro: IPR002343; Hud\_Sxl\_RNA.  
 DR InterPro: IPR000504; RNA\_rec\_mot.  
 DR Pfam: PF00076; rrm; 2.  
 DR PRINTS: PR00961; HDXSXLRNA.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PS50102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; 1.

KW RNA-binding; Repeat; Nuclear protein; Alternative splicing.  
 FT DOMAIN 85 163 RNA-BINDING (RRM) 1.  
 FT SMART: 171 251 RNA-BINDING (RRM) 2.  
 SQ SEQUENCE 307 AA; 33648 MW; 6F2C3DEFB85B8FC CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 307;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GYAFVD 7  
 DB 127 GYAFVD 132  
 RESULT 7  
 SOLR\_CLOAB STANDARD: PRT; 318 AA.  
 ID SOLR\_CLOAB P33746;  
 AC P33746;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE SOL locus transcriptional repressor.  
 GN SOLR OR CAP0161.  
 OS Clostridium acetobutylicum.  
 OC Clostridia; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_Taxid=1488;  
 [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RC MEDLINE-94042861; PubMed-822639;  
 RA Fischer R.J., Helms J., Duerte P.;  
 RT "Cloning, sequencing, and molecular analysis of the sol operon of  
 Clostridium acetobutylicum, a chromosomal locus involved in  
 solventogenesis.";  
 RT J. Bacteriol. 175:6959-6969(1993).  
 [2]  
 SEQUENCE FROM N.A.  
 RP STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RC MEDLINE-99084972; PubMed-9864345;  
 RA Nair R.V., Green E.M., Watson D.E., Bennett G.N., Papoutsakis E.T.;  
 RT "Regulation of the sol locus genes for butanol and acetone formation  
 in Clostridium acetobutylicum ATCC 824 by a putative transcriptional  
 repressor.";  
 RT J. Bacteriol. 181:319-330(1999).  
 [3]  
 SEQUENCE FROM N.A.  
 RP STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RC MEDLINE-21359325; PubMed-11466286;  
 RA Neilling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,  
 RA Tatusov R.L., Sabatln E.V., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 bacterium Clostridium acetobutylicum.";  
 RT J. Bacteriol. 183:4823-4838(2001).  
 -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF THE SOL LOCUS (ADHE/ADP,  
 CTFE, CTFB AND ADC) GENES FOR BUTANOL AND ACETONE FORMATION.  
 -1- SIMILARITY: CONTAINS 4 TPR REPEATS.  
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 CC EMBL: X72831; CA51342.1;  
 DR EMBL: L14817; ADO04637.1;  
 DR EMBL: AE001438; AAK76906.1;  
 DR PIR: S33433; S33433.

DR InterPro: IPR001440; TPR.  
 DR Pfam: PF00515; TPR; 5.  
 DR SMART: SM00028; TPR; 4.  
 KW Transcription regulation; Repressor; Repeat; TPR repeat; Plasmid;  
 KW Complete proteome.  
 FT REPEAT 65 98 TPR 1.  
 FT REPEAT 99 132 TPR 2.  
 FT REPEAT 133 166 TPR 3.  
 FT REPEAT 167 199 TPR 4.  
 SQ SEQUENCE 318 AA; 36939 MW; 49CED287FEE4FEF8 CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 ALKAIE 19  
 DB 223 ALKAIE 228  
 RESULT 8  
 FABH\_CAMJE STANDARD: PRT; 324 AA.  
 ID FABH\_CAMJE Q9P1H1;  
 AC Q9P1H1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41) (Beta-  
 DE ketoacyl-ACP synthase III) (KAS III).  
 GN FABH OR CJ0328C.  
 OS Campylobacter jejuni.  
 OS Campylobacteriaceae; Epsilon subdivision; Campylobacter group;  
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
 OC Campylobacter.  
 OX NCBI\_Taxid=197;  
 [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN-NCTC 11168;  
 RC MEDLINE-20150912; PubMed-10688204;  
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,  
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Pean C.W.,  
 RA Quail M.A., Rajandream A.M., Rutherford K.M., van Vliet A.H.M.,  
 RA Whitehead S., Barrett B.G.;  
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
 reveals hypervariable sequences.";  
 RT Nature 403:665-668(2000).  
 -1- FUNCTION: CATALYZES THE CONDENSATION REACTION OF FATTY ACID  
 SYNTHESIS BY THE ADDITION TO AN ACYL ACCEPTOR OF TWO CARBONS  
 FROM MALONYL-ACP. KAS III CATALYZES THE FIRST CONDENSATION  
 REACTION WHICH INITIATES FATTY ACID SYNTHESIS AND MAY THEREFORE  
 CC PLAY A ROLE IN GOVERNING THE TOTAL RATE OF FATTY ACID PRODUCTION.  
 CC POSSESSES BOTH ACETOACETYL-ACP SYNTHASE AND ACETYL TRANSACYLASE  
 CC ACTIVITIES (BY SIMILARITY).  
 -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-(acyl-  
 CC carrier protein) = 3-oxoacyl-[acyl-carrier protein] + Co(2) +  
 CC [acyl-carrier protein].  
 -1- PATHWAY: Fatty acid biosynthesis.  
 -1- SIMILARITY: BELONGS TO THE FABH FAMILY.  
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 CC EMBL: AL139074; CAB72795.1;  
 DR HSSP: P24249; 1HNK.  
 DR InterPro: IPR004655; FabH.  
 DR InterPro: IPR001099; N-C-synthase.  
 DR ProDom: PD000453; N-C-synthase; 1.  
 DR TIGRFAMs: TIGR00747; fabh; 1.



KM Fatty acid biosynthesis; Transferase; Acyltransferase;  
 KW Multifunctional enzyme; Complete proteome.  
 FT ACT\_SITE 114 114 BY SIMILARITY.  
 FT ACT\_SITE 246 246 BY SIMILARITY.  
 FT ACT\_SITE 276 276 BY SIMILARITY.  
 SQ SEQUENCE 324 AA: 35165 MW: BIDE49F08016D9E CRC64:

Query Match 31.6%; Score 6; DB 1; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKATE 19  
 Db 60 ALKATE 65

## RESULT 9

SYL\_MUSDO STANDARD: PRT: 324 AA.  
 ID SYL\_MUSDO  
 AC 017310: 017309.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sex-lethal protein homolog.  
 GN SYL.  
 OS Musca domestica (House fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Muscoidea; Muscidae; Musca.  
 NX NCBI\_TaxID=7570;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS SYL1 AND SYL2).  
 RC TISSUE=Ovary;  
 RX MEDLINE=98171463; PubMed=9502729;  
 RA Meise M., Hilfler-Kleiner D., Duebendorfer A., Brunner C.,  
 RA Noehliger R., Bopp D.;  
 RT "Sex-lethal, the master sex-determining gene in Drosophila, is not  
 sex-specifically regulated in Musca domestica."  
 RT Development 125:1487-1494(1998).  
 RL  
 CC -1- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX  
 DETERMINATION.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; SYL1 AND SYL2  
 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SOMATIC CELLS OF BOTH SEXES  
 THROUGHOUT DEVELOPMENT, BUT NOT IN THE POLE CELLS WHICH ARE THE  
 PROGENITORS OF THE GERMLINE.  
 CC -1- DEVELOPMENTAL STAGE: FIRST APPEARS IN BLASTODERM EMBRYOS AFTER  
 ONSET OF CELLULARISATION.  
 CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
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 CC  
 CC EMBL: AF025689; AAB81985.1; -  
 CC EMBL: AF025690; AAB81986.1; -  
 CC HSSP: P19339; 1SXL.  
 DR InterPro: IPR002343; Huo\_Sxl\_RNA.  
 DR InterPro: IPR000504; RNA\_rec-mot.  
 DR Pfam: PF00076; rrm; 2.  
 DR PRINTS: PR00961; HODSXLRNA.  
 DR SMART: SMO0360; RRM; 2.  
 DR PROSITE: PS50102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_Nuc\_1; 1.  
 KW RNA-binding; Repeat; Nuclear protein; Alternative splicing.  
 FT DOMAIN 102 180 RNA-BINDING (RRM) 1.  
 FT DOMAIN 188 268 RNA-BINDING (RRM) 2.  
 FT DOMAIN 88 94 POLY-GLY.

FT VANSPLIC 304 324 GRONKRNKHKVHPNPKKFI -> AVNYSGLIDFYNKKS  
 FT CONFLICT 8 9 IHTFTL (IN ISOFORM SYL1)  
 FT SEQUENCE 324 AA: 35755 MW: A65210E8A5CF67 CRC64;  
 SQ SEQUENCE 324 AA: 35755 MW: A65210E8A5CF67 CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVD 7  
 Db 144 GYAFVD 149

## RESULT 10

RECA\_THERM STANDARD: PRT: 340 AA.  
 ID RECA\_THERM  
 AC P48297; G9AGJ9;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE RecA protein (Recombinase A).  
 GN RECA.  
 OS Thermus thermophilus.  
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;  
 OC Thermaceae; Thermus.  
 NX NCBI\_TaxID=274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95014407; PubMed=7929298;  
 RA Wetmur J.G., Wong D.M., Ortiz B., Tong J., Reichert F., Gelfand D.H.;  
 RT Cloning, sequencing, and expression of RecA proteins from three  
 RT distantly related thermophilic bacteria."  
 RT J. Biol. Chem. 269:25928-25935(1994).  
 RL  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-HB8; ATCC 27634;  
 RX MEDLINE=94186518; PubMed=8138553;  
 RA Kato R., Kurimatsu S.;  
 RT "RecA protein from an extremely thermophilic bacterium, Thermus  
 RT thermophilus HB8."  
 RT J. Biochem. 114:926-929(1993).  
 RL  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-HB27;  
 RA Casares L., Castan P., Barbe J., Berenguer J.;  
 RT Analysis of the Thermus thermophilus HB27 RecA."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of  
 CC DNA by duplex DNA, and the ATP-dependent uptake of single-stranded  
 CC homologous single-stranded DNAs. It interacts with LexA causing  
 CC its activation and leading to its autocatalytic cleavage.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.  
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 CC  
 CC EMBL: U03058; AAM4935.1; -  
 CC EMBL: D17392; BAA04215.1; -  
 CC EMBL: AF31800; AAK13521.1; -  
 CC HSSP: F26345; 1G19.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR001553; RECA.  
 DR Pfam: PF00154; RECA; 1.  
 DR PRINTS: PR00142; RECA.  
 DR ProDom: PD000229; RECA; 1.

DR SMART: SM00382; AAA: 1.  
 DR PROSITE: PS00321; RECA\_1; 1.  
 DR PROSITE: PS50162; RECA\_2; 1.  
 DR PROSITE: PS50163; RECA\_3; 1.  
 KM DNA damage: DNA recombination: SOS response; ATP-binding; DNA-binding.  
 FT BINDING 65 72  
 FT CONFLICT 151 155 A -> G (IN REF. 3).  
 FT CONFLICT 239 239 G -> A (IN REF. 3).  
 FT CONFLICT 321 321 A -> T (IN REF. 3).  
 FT CONFLICT 327 329 SDG -> AGE (IN REF. 3).  
 SO SEQUENCE 340 AA: 36385 MW: 53f4A4A2F54B2BD4 CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 14 ALKAIE 19  
 Db 12 ALKAIE 17  
 RESULT 11  
 SXL\_CERCA STANDARD: PRT: 348 AA.  
 ID SXL\_CERCA  
 AC P51374  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sex-lethal protein homolog (CCSXL).  
 GN SXL.  
 OS Ceratitis capitata (Mediterranean fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Tephritidae; Tephritidae; Ceratitis.  
 OX NCBI\_TaxID=7213;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Benkeleon; PubMed=9502730;  
 RA Saccone G., Peluso I., Arliccio D., Giordano E., Bopp D., Pollito L.C.;  
 RT The Ceratitis capitata homologue of the Drosophila sex-determining  
 RT gene sex-lethal is structurally conserved, but not sex-specifically  
 RT developed. 125:1495-1500(1998).  
 RL Development.  
 CC -1- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX  
 CC DETERMINATION.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS: ADULT-SPECIFIC ISOFORMS  
 CC AL, A2, A3, A4, AND EMBRYO-SPECIFIC ISOFORMS E1, E2 AND E3 (SHOWN  
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYOS OF BOTH SEXES. ALSO  
 CC EXPRESSED IN THE PROGENITOR CELLS OF THE GERMLINE.  
 CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
 CC  
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 CC  
 CC EMBL: AF026145; AAC38966.1; -.  
 DR HSSP: P19339; ISXL.  
 DR InterPro: IPR000504; RNA\_rec\_mot.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PS50102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
 KM RNA-binding: Repeat; Nuclear protein; Alternative splicing.  
 KW DOMAIN 1 27 GLY/ASN-RICH DOMAIN.  
 FT DOMAIN 110 188 RNA-BINDING (RRM) 1.

FT DOMAIN 196 276 RNA-BINDING (RRM) 2.  
 FT DOMAIN 68 75 POLY-GLY.  
 FT DOMAIN 95 99 POLY-GLY.  
 FT DOMAIN 293 311 POLY-GLY.  
 FT DOMAIN 312 316 POLY-PRO.  
 FT VARSPLIC 37 44 MISSING (IN ISOFORM A1).  
 SO SEQUENCE 348 AA: 37188 MW: CAB5D5C2C8674A CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 GYAFVD 7  
 Db 152 GYAFVD 157  
 RESULT 12  
 ISPG\_CLOPE STANDARD: PRT: 349 AA.  
 ID ISPG\_CLOPE  
 AC P58667;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.  
 DE 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.  
 OS Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-13 / Type A;  
 RA PubMed=1192842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,  
 RA Shiba T., Ogawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -1- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate  
 CC (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate  
 CC (by similarity).  
 CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.  
 CC -1- SIMILARITY: BELONGS TO THE ISPG FAMILY.  
 CC  
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 CC  
 CC EMBL: AF003191; BAB81398.1; -.  
 DR InterPro: IPR004588; GCPE.  
 DR InterPro: IPR000660; Ntr\_Sir.  
 DR Pfam: PF01077; Ntr\_Sir; 1.  
 DR TIGRPFAMs: TIGR00612; gcpe; 1.  
 KM Isoprene biosynthesis; Complete proteins.  
 SO SEQUENCE 349 AA: 38017 MW: FC4B95B8775B0343 CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 14 ALKAIE 19  
 Db 88 ALKAIE 93  
 RESULT 13  
 SXL\_DROME STANDARD: PRT: 354 AA.  
 ID SXL\_DROME

AC P19339; P19340; Q99141; Q9TYF5; Q26466; Q9W3S6;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sex-lethal protein.  
 GN SXL OR SX1 OR CG18350.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS MS3 AND CM1).  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=89077532; PubMed=3144435;  
 RA Bell L.R., Maine E.M., Schedl P., Cline T.W.;  
 RT "Sex-lethal, a Drosophila sex determination switch gene, exhibits sex-specific RNA splicing and sequence similarity to RNA binding proteins.";  
 RT Cell 55:1037-1046(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS MS3; MS11 AND MS16).  
 RC TISSUE=Embryo;  
 RX MEDLINE=91260708; PubMed=1710769;  
 RA Samuels M.E., Schedl P., Cline T.W.;  
 RT "The complex set of late transcripts from the Drosophila sex determination gene sex-lethal encodes multiple related polypeptides.";  
 RT Mol. Cell. Biol. 11:3584-3602(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS MS3; MS11 AND CM1).  
 RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G.G., Nelson C.R., Miklos G.L.G., Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman J.P., Bhandal D., Bolshakov S., Borkan D., Botchan M.R., Bouck J., Brokstein P., Brotlier P., Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C., Juelai B., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paigled J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Splet E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-T., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L., Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RT Science 287:2185-2195(2000).  
 RN [4]  
 RP SEQUENCE OF 1-26 FROM N.A. (ISOFORM EMBRYO-SPECIFIC).

RC TISSUE=Embryo;  
 RX MEDLINE=92191272; PubMed=1547493;  
 RA Keyes L.N., Cline T.W., Schedl P.;  
 RT "The primary sex determination signal of Drosophila acts at the level of transcription.";  
 RT Cell 68:933-943(1992).  
 RN [5]  
 RP SEQUENCE OF 1-41 FROM N.A. (ISOFORM FEMALE-SPECIFIC).  
 RX MEDLINE=97132600; PubMed=8978052;  
 RA Sakamoto H., Inoue K., Higuchi I., Ono Y., Shimura Y.;  
 RT "Regulation of the gene Sex-lethal: a comparative analysis of Drosophila melanogaster and Drosophila subobscura.";  
 RT Genetics 144:1653-1664(1996).  
 RN [6]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93087158; PubMed=1454517;  
 RA Sakamoto H., Inoue K., Higuchi I., Ono Y., Shimura Y.;  
 RT "Control of Drosophila sex-lethal pre-mRNA splicing by its own female-specific product.";  
 RT Nucleic Acids Res. 20:5533-5540(1992).  
 RN [7]  
 RP STRUCTURE BY NMR OF 199-294.  
 RX MEDLINE=95034815; PubMed=7524663;  
 RA Lee A.L., Kanaar R., Rio D.C., Wemmer D.E.;  
 RT "Resonance assignments and solution structure of the second RNA-binding domain of sex-lethal determined by multidimensional heteronuclear magnetic resonance.";  
 RT Biochemistry 33:13775-13786(1994).  
 RN [8]  
 RP STRUCTURE BY NMR OF 122-209.  
 RX MEDLINE=97446155; PubMed=9299339;  
 RA Inoue M., Muto Y., Sakamoto H., Kigawa T., Takio K., Shimura Y., Yokoyama S.;  
 RT "A characteristic arrangement of aromatic amino acid residues in the solution structure of the amino-terminal RNA-binding domain of Drosophila sex-lethal.";  
 RT J. Mol. Biol. 273:82-94(1997).  
 CC -!- FUNCTION: SEX DETERMINATION SWITCH PROTEIN WHICH CONTROLS SEXUAL DEVELOPMENT BY SEX-SPECIFIC SPLICING. REGULATES DOSAGE COMPENSATION IN FEMALES BY SUPPRESSING HYPERACTIVATION OF X-LINKED GENES. EXPRESSION OF THE EMBRYO-SPECIFIC ISOFORM IS UNDER THE CONTROL OF X PRIMARY SEX-DETERMINING SIGNAL, WHICH DEPENDS ON THE RATIO OF X CHROMOSOMES RELATIVE TO AUTOSOMES (X:A RATIO). EXPRESSION OCCURS IN 2X:2A CELLS, BUT NOT IN X:2A CELLS. THE X:A RATIO SEEMS TO BE SIGNALLED BY THE RELATIVE CONCENTRATION OF THE X-LINKED TRANSCRIPTION FACTORS SIS-A AND SIS-B. AS A RESULT, THE EMBRYO-SPECIFIC PRODUCT IS EXPRESSED EARLY ONLY IN FEMALE EMBRYOS AND SPECIFIC FEMALE-ADULT SPECIFIC SPLICING; IN THE MALE WHERE IT IS NOT EXPRESSED, THE DEFAULT SPLICING GIVES RISE TO A TRUNCATED NONFUNCTIONAL PROTEIN. THE FEMALE-SPECIFIC ISOFORM SPECIFIES THE SPLICING OF ITS OWN TRANSCRIPT, THEREBY INITIATING A POSITIVE AUTOREGULATORY FEEDBACK LOOP LEADING TO FEMALE DEVELOPMENT PATHWAY. THE FEMALE-SPECIFIC ISOFORM CONTROLS THE SEX-SPECIFIC SPLICING OF TRANSFORMER (TRA); ACTS AS A TRANSLATIONAL REPRESSOR FOR MALE-SPECIFIC LETHAL-2 (MSL-2) AND PREVENTS MALE-LESS (MLE), MSL-1 AND MSL-3 PROTEINS FROM ASSOCIATING WITH THE FEMALE X CHROMOSOME.  
 CC -!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS: EMBRYO-SPECIFIC, MALE-SPECIFIC CM1, FEMALE-SPECIFIC MS3/CF1 (SHOWN HERE), FEMALE-SPECIFIC MS11 AND FEMALE-SPECIFIC MS16; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN SOMATIC TISSUES, BUT NOT IN THE POLE CELLS, WHICH ARE THE PRECURSORS OF THE GERMLINE.  
 CC -!- DEVELOPMENTAL STAGE: THE EMBRYO-SPECIFIC ISOFORM IS EXPRESSED FOR A BRIEF PERIOD DURING THE SYNCTIAL BLASTODERM STAGE. THE MALE-SPECIFIC MS11 ISOFORM IS EXPRESSED IN 4-7 HOURS EMBRYO.  
 CC -!- DOMAIN: THE GLY-ASN RICH DOMAIN IS REQUIRED FOR THE COOPERATIVE INTERACTION WITH RNA AND FOR REGULATING THE SPLICING ACTIVITY.  
 CC -!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
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Search completed: April 16, 2003, 16:35:24  
 Job time : 5.96716 secs

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FT DOMAIN 314 321 POLY-PRO.
FT VARSPLIC 1 25 MYGNNGPNNNGGPPGYNKSS -> MDPSEYTPPC
FT RPRGRITISRMQ (IN ISOFORM EMBRYO-
FT VARSPLIC 26 59 SPECIFIC).
FT GGRGFGMSHSLPSCGMSRYARSPDTEFSPSSSS -> SFH
FT SYGAGVTACPPSKSRNRRFRQKRDTRNS (IN
FT ISOFORM MALE-SPECIFIC).
FT VARSPLIC 60 354 MISSING (IN ISOFORM MALE-SPECIFIC).
FT VARSPLIC 41 48 MISSING (IN SOME CLONES).
SO SEQUENCE 354 AA; 38715 MW; 760347AEF4DB7868 CRC64;
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Query Match 31.6%; Score 6; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2 GYAFVD 7
    |||||
Db 169 GYAFVD 174
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RESULT 15
ISPG_BACHD STANDARD: PRT: 367 AA.
ID ISPG_BACHD
AC O9KD18;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.
GN ISPG OR GCPE OR BH1401.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -i- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate
CC (ME-2,4cpP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC (by similarity)
CC -i- PATHWAY: Nonnevalonate terpenoid biosynthesis pathway; sixth step.
CC -i- SIMILARITY: BELONGS TO THE ISPG FAMILY.
CC -----
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CC -----
DR EMBL: AP001511; BAB05120.1;
DR InterPro: IPR004588; GCPE.
DR InterPro: IPR000660; NIT_SIR.
DR Pfam: PF01077; NIT_SIR; 1.
DR TIGRFAMs: TIGR00612; GCPE; 1.
DR Isoprene biosynthesis; Complete proteome.
SO SEQUENCE 367 AA; 39581 MW; 217DD02965AMD2AD CRC64;
```

```

Query Match 31.6%; Score 6; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 14 ALKATE 19
    |||||
Db 92 ALKATE 97
```



GenCore version 5.1.4-p5\_4578  
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## OM protein - protein search, using sw model

Run on: April 16, 2003, 16:30:00 ; Search time 2.3087 Seconds

(without alignments)  
1695.712 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 19  
Sequence: 1 TGVAFVDCPDSEWALKATE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_podent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	579	4 000425	000425 homo sapien
2	11	57.9	100	11 09B054	09B054 mus musculu
3	11	57.9	579	11 09CPN8	09CPN8 mus musculu
4	10	52.6	576	13 042254	042254 gallus gall
5	10	52.6	577	4 09N218	09N218 mus sapien
6	10	52.6	577	11 088477	088477 mus musculu
7	10	52.6	582	13 09PW80	09PW80 brachydanto
8	10	52.6	594	13 057526	057526 xenopus lae
9	10	52.6	594	13 079332	079332 xenopus lae
10	7	36.8	310	2 P96562	P96562 amycolators
11	7	36.8	337	2 052816	052816 amycolators
12	7	36.8	404	2 09X324	09X324 bacillus an
13	7	36.8	406	2 087675	087675 amycolators
14	7	36.8	406	2 08RM03	08RM03 amycolators
15	7	36.8	653	5 09VX29	09VX29 dirosophila
16	7	36.8	663	5 085Y03	085Y03 dirosophila

17	6	31.6	114	10 09M455	09M455 elaeis guin
18	6	31.6	116	12 09MMY9	09MMY9 dioscorea a
19	6	31.6	147	16 09CH22	09CH22 lactococcus
20	6	31.6	156	17 09HQX9	09HQX9 halobacteri
21	6	31.6	178	16 025351	025351 helicobacte
22	6	31.6	178	16 09ZLK2	09ZLK2 helicobacte
23	6	31.6	188	16 09KCM7	09KCM7 bacillus ha
24	6	31.6	204	2 09F8G6	09F8G6 carboxydoth
25	6	31.6	222	10 09MJJ2	09MJJ2 arabidopsis
26	6	31.6	225	10 08S303	08S303 nicotiana b
27	6	31.6	234	16 08UGF6	08UGF6 agrobacteri
28	6	31.6	244	16 0981F4	0981F4 rhizobium l
29	6	31.6	250	16 08X0B0	08X0B0 raietonia s
30	6	31.6	257	16 034744	034744 bacillus su
31	6	31.6	268	2 09LCS2	09LCS2 azotobacter
32	6	31.6	286	16 09BR40	09BR40 mycoplasma
33	6	31.6	287	16 08Z1U5	08Z1U5 salmonella
34	6	31.6	287	16 08Z310	08Z310 salmonella
35	6	31.6	313	17 09HP19	09HP19 halobacteri
36	6	31.6	319	5 09U2W8	09U2W8 caenorhabdi
37	6	31.6	324	5 09BKX4	09BKX4 lucilia cup
38	6	31.6	325	5 09BKX3	09BKX3 lucilia cup
39	6	31.6	328	16 09ZSD9	09ZSD9 rhizobium m
40	6	31.6	340	16 09ZM14	09ZM14 yerinia pe
41	6	31.6	342	3 0967M5	0967M5 coccidioid
42	6	31.6	344	16 0835S6	0835S6 treponema p
43	6	31.6	374	17 08U205	08U205 pyrococcus
44	6	31.6	386	16 08XK16	08XK16 gliostictidum
45	6	31.6	397	5 023561	023561 caenorhabdi

## ALIGNMENTS

RESULT 1  
ID 000425 PRELIMINARY: PRT: 579 AA.  
AC 000425:  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Putative RNA binding protein KOC (KOC).  
GN KOC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Mueller-Pillasch F., Lacher U., Wallrapp C., Et AL.:  
RL Oncogene 0:0-0(0).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANCREAS;  
RA Mueller-Pillasch F., Lacher U., Wallrapp C.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U76705; AAC3208.1; -  
DR EMBL: U76705; AAC09223.1; -  
DR InterPro: IPR004087; KH\_dom.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF00013; KH-domain; 4.  
DR Pfam: PF00076; rim; 2.  
DR SMART: SM00322; KH; 4.  
DR SMART: SM00360; RRM; 2.  
DR PROSITE: PS50084; KH\_type\_1; 4.  
DR PROSITE: PS50102; RRM; 2.  
DR PROSITE: PS00030; RRM\_RNP\_1; FALSE NEG.  
SQ SEQUENCE 579 AA: 63720 MW: AEECA3BER3C135C5 CRC64:  
Query Match 100.0%; Score 19; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

```
OY 1 TGYAFVDCPDE 19
DB 37 TGYAFVDCPDE 55

RESULT 2
ID 09D054 PRELIMINARY: PRT: 100 AA.
AC 09D054
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 2610101N1IRAK protein.
GN IGF2BP3 OR 2610101N1IRAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fritschmann M., Gaasterland T., Last C., Ring B., Gough J.,
RA Fritschmann M., Gaasterland T., Last C., Ring B., Gough J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
RA Hayashizaki Y.,
RA Functional annotation of a full-length mouse cDNA collection."
RT Nucleotide 6902001.
DR EMBL: AK01797.60284.1.
DR MGD: MGI:1890359.197283.1.
DR InterPro: IPR00504. RNA_rec_mot.
DR Pfam: PF00076. rrm. 1.
DR SMART: SM00360. RRM. 1.
DR PROSITE: PS50102. RRM. 1.
SQ SEQUENCE 100 AA: 11249 MW: 4D871E37EB9D5466 CRC64;

Query Match 57.9%; Score 11; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDE 11
DB 37 TGYAFVDCPDE 47

RESULT 3
ID 09C9N8 PRELIMINARY: PRT: 579 AA.
AC 09C9N8
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 10 days embryo cDNA. RIKEN full-length enriched library,
DE clone:2610036B18, full insert sequence (Igf2 mRNA-binding protein
DE 3).
GN IGF2BP3 OR 2610101N1IRAK OR MIM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fritschmann M., Gaasterland T., Last C., Ring B., Gough J.,
RA Fritschmann M., Gaasterland T., Last C., Ring B., Gough J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
RA Hayashizaki Y.,
RA Functional annotation of a full-length mouse cDNA collection."
RT Nucleotide 409:685-690(2001).
DR EMBL: AK01797.60284.1.
DR MGD: MGI:1890359.197283.1.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR00504; RNA_rec_mot.
DR Pfam: PF00076. rrm. 2.
DR SMART: SM00360. RRM. 2.
DR PROSITE: PS50084. KH_type_1.
DR PROSITE: PS50102. RRM. 1.
DR PROSITE: PS50102. RRM. 1.
SQ SEQUENCE 579 AA: 63574 MW: CABD9A435B39287 CRC64;

Query Match 57.9%; Score 11; DB 11; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDE 11
DB 37 TGYAFVDCPDE 47

RESULT 4
ID 042254 PRELIMINARY: PRT: 576 AA.
AC 042254
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE zipcode-binding protein.
GN zbp1.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Gallusgallus; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
NCBI_TaxID=9031.
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=97220007; PubMed=9121465;
```



RA Ross A.F., Oleynikov Y.S., Kislauskis E.H., Taneja K.L., Singer R.H.;  
 RT "Characterization of a beta-actin mRNA zipcode-binding protein.";  
 RL Mol. Cell. Biol. 17:2158-2165(1997).  
 DE EMBL: AF026527; AAB82295.1; -  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rtm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PSS0030; RRM\_RNP\_1; FALSE\_NEG.  
 DR PROSITE: PSS0102; RRM; 2.  
 SQ SEQUENCE 576 AA; 63271 MW; 01AAF2D1D81C8811 CRC64;

Query Match 52.6%; Score 10; DB 13; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GYAFVDCPDE 11  
 |||||  
 Db 38 GYAFVDCPDE 47

## RESULT 5

OQNZ18 PRELIMINARY; PRT; 577 AA.

AC OQNZ18;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE mRNA-binding protein CRDBP.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RA Ioannidis P., Trangas T., Dimitriadis E., Samiotaki M.,  
 RA Panoutsakopoulos G., Kyriazoglou I., Voutzoulis S., Tsilipalis C.M.,  
 RA Kittas C., Agnantis N., Pandis N.;  
 RT "Pectopic expression of a KH-domain containing protein, highly  
 RT homologous to both human IMP-1 and mouse CRD-BP, in benign and  
 RT malignant mesenchymal tumors.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF198254; AAF37203.1; -  
 DR HSSP: P11940; 1CVJ.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rtm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PSS0102; RRM; 2.  
 SQ SEQUENCE 577 AA; 63456 MW; 0749A060F252D81D CRC64;

Query Match 52.6%; Score 10; DB 4; Length 577;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GYAFVDCPDE 11  
 |||||  
 Db 38 GYAFVDCPDE 47

## RESULT 6

O88477 PRELIMINARY; PRT; 577 AA.

AC O88477;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Coding region determinant binding protein (Coding region determinant-  
 DE binding protein).  
 GN IGF2BP1 OR CRDBP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9221743; PubMed=1559612;  
 RA Bernstein P.L., Herrick D.J., Prokipack R.D., Ross J.;  
 RT "Control of c-myc mRNA half-life in vitro by a protein capable of  
 RT binding to a coding region stability determinant.";  
 RL Genes Dev. 6:642-654(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9415886; PubMed=8114742;  
 RA Herrick D.J., Ross J.;  
 RT "The half-life of c-myc mRNA in growing and serum-stimulated cells:  
 RT Influence of the coding and 3' untranslated regions and role of  
 RT ribosome translocation.";  
 RL Mol. Cell. Biol. 14:2119-2128(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94179348; PubMed=8132663;  
 RA Prokipack R.D., Herrick D.J., Ross J.;  
 RT "Purification and properties of a protein that binds to the C-terminal  
 RT coding region of human c-myc mRNA.";  
 RL J. Biol. Chem. 269:9261-9269(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9732234; PubMed=9178888;  
 RA Leeds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.,  
 RA Gruppiso P.A., Ross J.;  
 RT "Developmental regulation of CRD-BP, an RNA-binding protein that  
 RT stabilizes c-myc mRNA in vitro.";  
 RL Oncogene 14:1279-1286(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Ross J., Prokipack R.D., Leeds P., Doyle G.A.R., Betz N.A.,  
 RA Fleisig A.J.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;  
 RX MEDLINE=21085660; PubMed=11217651;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schram L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,  
 RA Blake J., Botfelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AF061569; AAC72743.1; -  
 DR EMBL: AK013940; BAB29071.1; -  
 DR HSSP: P11940; 1CVJ.  
 DR MGD: MGI:1890357; Igf2bp1.  
 DR InterPro: IPR004087; KH\_dom.



DR SMART: SM00322; KH: 4.  
 DR SMART: SM00360; RRM: 2.  
 DR PROSITE: PS50084; KH\_TYPE\_1: 4.  
 DR PROSITE: PS50102; RRM: 2.  
 SQ SEQUENCE 594 AA; 65643 MW; 54CEA7BEF0856DD6 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 10; DB 13; Length 594;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVDCPD 11  
 |||||  
 DB 38 GYAFVDCPD 47

RESULT 10  
 P96562 PRELIMINARY; PRT; 310 AA.

AC P96562:  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Putative cytochrome P450 165C2 (Hypothetical hydroxylase D) (Fragment).  
 DE CYP165C2.  
 GN CYP165C2.  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C329.4;  
 RA Solenberg P.J., Matsushima P., Stack D.R., Wilkie S.C., Thompson R.C.,  
 RA Bultz R.H.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL: U84350; ABA49296.1; -  
 DR HSSP: 000441; 10XA;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 KW Electron transport; Heme; Hypothetical protein; Membrane;  
 KW Monooxygenase; Oxidoreductase.  
 FT NON\_TER 1  
 FT BINDING 1  
 FT SEQUENCE 310 AA; 34255 MW; 0155572AP694487 CRC64;  
 SQ SEQUENCE 310 AA; 34255 MW; 0155572AP694487 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 310;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPD 10  
 |||||  
 DB 298 AFVDCPD 304

RESULT 11  
 O52816 PRELIMINARY; PRT; 337 AA.

AC 052816:  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE PC2A361.27 (Fragment).  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Wageningen A., Kirkpatrick P., Williams D., Harris B., Kershaw J.,  
 RA Leonard N., Jones M., Jones S., Solenberg P.;  
 RT \*Sequencing and analysis of genes involved in the biosynthesis of a

RT vancomycin group antibiotic.";  
 RL Chem. Biol. 3:155-162(1998).  
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL: AJ223998; CA11791.1; -  
 DR HSSP: Q00441; 10XA.  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 FT NON\_TER 1  
 FT SEQUENCE 337 AA; 37418 MW; 75A3729A01C8CB89 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 337;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPD 10  
 |||||  
 DB 325 AFVDCPD 331

RESULT 12  
 O9X324 PRELIMINARY; PRT; 404 AA.

AC O9X324:  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PX01-54.  
 OS Bacillus anthracis.  
 OC Plasmid virulence plasmid PX01.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STERNE;  
 RL MEDLINE=99445483; PubMed=10515943;  
 RA Oklnaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.R.,  
 RA Kelm P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,  
 RA Martinez Y., Rieke D., Svensson R., Jackson P.J.;  
 RT "Sequence and organization of PX01, the large Bacillus anthracis  
 RT plasmid harboring the anthrax toxin genes.";  
 RL J. Bacteriol. 181:6509-6515(1999).  
 DR EMBL: AF065404; AAD32358.1; -  
 DR InterPro: IPR001119; SLH.  
 DR Pfam: PF00395; SLH.3.  
 DR PROSITE: PS01072; SLH\_DOMAIN; UNKNOWN\_1.  
 DR Plasmid.  
 SQ SEQUENCE 404 AA; 45044 MW; 45D08FAA450C0C4C CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 404;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SWALKAI 18  
 |||||  
 DB 175 SWALKAI 181

RESULT 13  
 O87675 PRELIMINARY; PRT; 406 AA.

AC 087675:  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Cytochrome P450 165C1 (Oxygenase C).  
 GN CYP165C1 OR OXYC.  
 OS Amycolatopsis mediterranei (Nocardia mediterranei).  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=33910;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DSM 5908;  
 RA Pelzer S., Stuessmuth R., Heckmann D., Recktenwald J., Huber P.,  
 RT Jung G., Wohlleben W.;  
 RT Identification and analysis of a glycopeptide biosynthetic gene  
 cluster and its use for manipulating balhimycin biosynthesis in the  
 RT producing organism Amycolatopsis mediterranei DSM5908.  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL: Y16952; CA76549.1; -;  
 DR HSPB: 000441; 10XA;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450; 1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 KW Heme; Monooxygenase; oxidoreductase.  
 SQ SEQUENCE 406 AA; 44795 MW; 203C2AC5293A0F13 CRC64;

Query Match 36.8%; Score 7; DB 2; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPD 10  
 |||||  
 Db 394 AFVDCPD 400

## RESULT 14

OBRN03 PRELIMINARY; PRT; 406 AA.  
 AC OBRN03;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE OYXC;  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.  
 OX NCBI\_TaxID:31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Zerbe K., Vrijsdied J.W., Robinson J.A.;  
 RT "DNA sequence coding for P450 monooxygenases of vancomycin producer  
 RT Amycolatopsis orientalis."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF486630; AAL90879.1; -;  
 SO SEQUENCE 406 AA; 45187 MW; 6C0E2EFA167A747A CRC64;

Query Match 36.8%; Score 7; DB 2; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPD 10  
 |||||  
 Db 394 AFVDCPD 400

## RESULT 15

OBYX29 PRELIMINARY; PRT; 653 AA.  
 AC OBYX29;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE CG12990 protein.  
 GN CG12990.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Gelinkier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Miklos G.L.G.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,  
 RA April J.F., Aspray A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houson K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kenson J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McKernson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
 RA Palazzolo M., Pittman K.A., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 DR EMBL: AE003506; AAF48752.1; -;  
 DR FLYbase: FBgn030859; CG12990.  
 DR InterPro: IPR002656; Acyl\_transf\_3.  
 DR Pfam: PF01757; Acyl\_transf\_3; 1.  
 SO SEQUENCE 653 AA; 74962 MW; 260525FDEA1B3856 CRC64;

Query Match 36.8%; Score 7; DB 5; Length 653;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SWALKAI 18  
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 Db 60 SWALKAI 66

Search completed: April 16, 2003, 16:36:39  
 Job time : 4.3087 secs

GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:18:40 : Search time 1.06076 Seconds

(without alignments)  
527.016 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 106

Sequence: 1 TGTATVDCPDSEWALKAE 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/6C.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	106	100.0	579 4 US-09-643-597-176	Sequence 176, App
2	106	100.0	579 4 US-09-643-597-176	Sequence 348, App
3	95	89.6	577 4 US-09-261-855-2	Sequence 2, Appli
4	48.5	45.8	309 3 US-09-109-205-1	Sequence 1, Appli
5	47	44.3	414 1 US-07-667-276A-4	Sequence 6, Appli
6	43	40.6	391 1 US-08-602-010A-6	Sequence 6, Appli
7	43	40.6	391 1 US-08-680-726A-6	Sequence 6, Appli
8	43	40.6	391 1 US-09-092-409-6	Sequence 6, Appli
9	42	39.6	885 4 US-09-342-648-9	Sequence 9, Appli
10	41.5	39.2	932 4 US-08-887-534A-45	Sequence 45, Appli
11	41	38.7	690 4 US-09-422-869-28	Sequence 28, Appli
12	41	38.7	759 1 US-08-676-967-1	Sequence 1, Appli
13	41	38.7	759 1 US-08-676-974-1	Sequence 1, Appli
14	41	38.7	759 2 US-09-098-487-1	Sequence 1, Appli
15	41	38.7	826 4 US-09-564-805-2	Sequence 2, Appli
16	41	38.7	826 4 US-09-564-805-224	Sequence 224, App
17	41	38.7	826 4 US-09-564-805-226	Sequence 226, App
18	40.5	38.2	333 3 US-09-188-579-80	Sequence 80, Appli
19	40.5	38.2	333 3 US-09-315-444-80	Sequence 80, Appli
20	40.5	38.2	333 4 US-09-721-362-80	Sequence 80, Appli
21	40.5	38.2	837 4 US-09-564-805-228	Sequence 228, App
22	40	37.7	72 4 US-08-973-273-27	Sequence 27, Appli
23	40	37.7	80 1 US-07-881-075-10	Sequence 10, Appli
24	40	37.7	80 1 US-08-120-827-10	Sequence 10, Appli
25	40	37.7	80 1 US-08-478-675-10	Sequence 10, Appli
26	40	37.7	336 1 US-07-667-276A-8	Sequence 8, Appli
27	40	37.7	398 1 US-08-261-822A-16	Sequence 16, Appli

28	40	37.7	398 5	PCF-US95-07744A-16	Sequence 16, Appli
29	40	37.7	519 4	US-09-312-183A-3	Sequence 3, Appli
30	40	37.7	547 4	US-09-312-183A-2	Sequence 2, Appli
31	40	37.7	822 4	US-09-564-805-222	Sequence 222, App
32	39	36.8	267 4	US-08-818-112-71	Sequence 71, Appli
33	39	36.8	267 4	US-08-818-111-72	Sequence 72, Appli
34	39	36.8	267 4	US-09-056-556-71	Sequence 71, Appli
35	39	36.8	267 4	US-09-072-596-72	Sequence 72, Appli
36	39	36.8	381 2	US-08-858-052-3	Sequence 3, Appli
37	39	36.8	381 3	US-09-200-284-3	Sequence 3, Appli
38	39	36.8	906 1	US-08-094-889-1	Sequence 9, Appli
39	38.5	36.3	566 3	US-08-325-8657-21	Sequence 21, Appli
40	38.5	36.3	593 3	US-08-104-282B-33	Sequence 33, Appli
41	38	35.8	57 2	US-08-845-623-33	Sequence 33, Appli
42	38	35.8	57 3	US-08-815-927-33	Sequence 33, Appli
43	38	35.8	57 4	US-09-103-330-33	Sequence 33, Appli
44	38	35.8	57 4	US-09-435-242-33	Sequence 33, Appli
45	36	35.8	57 4	US-09-435-242-33	Sequence 33, Appli

## ALIGNMENTS

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Result 1
US-09-643-597-176
Sequence 176, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-176

Query Match          100.0%: Score 106; DB 4; Length 579;
Best Local Similarity 100.0%: Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTATVDCPDSEWALKAE 19
DB 37 TGTATVDCPDSEWALKAE 55

RESULT 2
US-09-643-597-348
Sequence 348, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.

```

```

? APPLICANT: Wang, Aljun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.455C11
? CURRENT APPLICATION NUMBER: US/09/643,597
? CURRENT FILING DATE: 2000-08-21
? NUMBER OF SEQ ID NOS: 369
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 348
? LENGTH: 579
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-643-597-348

Query Match
Best Local Similarity 100.0%; Score 106; DB 4; Length 579;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDSESMALKAE 19
DB 37 TGTAFTVDCPDSESMALKAE 55

RESULT 3
? Sequence 2, Application US/09261855A
? Patent No. 6255055
? GENERAL INFORMATION:
? APPLICANT: Ross, Jeffrey
? TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
? FILE REFERENCE: 960296.95131
? CURRENT APPLICATION NUMBER: US/09/261,855A
? CURRENT FILING DATE: 1999-03-03
? NUMBER OF SEQ ID NOS: 46
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 2
? LENGTH: 577
? TYPE: PRT
? ORGANISM: Mus musculus
? US-09-261-855-2

Query Match
Best Local Similarity 89.68; Score 95; DB 4; Length 577;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDSESMALKAE 19
DB 37 SGTAFTVDCPDSESMALKAE 55

RESULT 4
? Sequence 1, Application US/09109205
? Patent No. 6057140
? GENERAL INFORMATION:
? APPLICANT: Lal, Preeti
? APPLICANT: Guegler, Karl J.
? APPLICANT: Gorgone, Gina
? APPLICANT: Corley, Neil C.
? APPLICANT: Baughn, Mariah R.
? APPLICANT: Yue, Henry
? TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Inocyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA

? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: Windows
? SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/109,205
? FILING DATE: Herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Cerrone, Michael C
? REGISTRATION NUMBER: 39,132
? REFERENCE/DOCKET NUMBER: PF-0542 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-855-0555
? TELEFAX: 650-855-0572
? TELEX:
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 309 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: LUNGNOT14
? CLONE: 1511003

? US-09-109-205-1

Query Match
Best Local Similarity 45.8%; Score 48.5; DB 3; Length 309;
Matches 11; Conservative 1; Mismatches 5; Indels 13; Gaps 1;

QY 1 TGTAFTVDCPDSESMALKAE 19
DB 130 TGKFFLDCPDSESMALKAE 159

RESULT 5
? Sequence 4, Application US/07667276A
? Patent No. 5470971
? GENERAL INFORMATION:
? APPLICANT: Kondo, Keiji
? APPLICANT: Inouye, Masayori
? TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
? OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Welser & Associates
? STREET: 230 S. Fifteenth Street, Suite 500
? CITY: Philadelphia
? STATE: PA
? COUNTRY: USA
? ZIP: 19102
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/667,276A
? FILING DATE: 11-MAR-1991
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Welser, Gerard J.
? REGISTRATION NUMBER: 19,763
? REFERENCE/DOCKET NUMBER: 377,5351P
? TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-667-276A-4

Query Match 44.3%; Score 47; DB 1; Length 414;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYAFVDCPDSEWALKATE 19  
DB 210 GYGVDFENKSYAEKATQ 227

RESULT 6  
US-08-602-010A-6  
Sequence 6, Application US/08602010A  
Patent No. 5753235

GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
ATTORNEY: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,010A  
FILING DATE: February 15, 1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-602-010A-6

Query Match 40.6%; Score 43; DB 1; Length 391;  
Best Local Similarity 42.1%; Pred. No. 47;  
Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 3 YAFVNC--PDSEWALKATE 19  
DB 153 YAVVSCWPEPSMKPECLE 171

RESULT 7  
US-08-680-726A-6  
Sequence 6, Application US/08680726A  
Patent No. 5604197  
GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.  
ATTORNEY: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/680,726A  
FILING DATE: 12-JUL-1996  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-680-726A-6

Query Match 40.6%; Score 43; DB 1; Length 391;  
Best Local Similarity 42.1%; Pred. No. 47;  
Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 3 YAFVDC--PDSEWALKATE 19  
DB 153 YAVVSCWPEPSMKPECLE 171

RESULT 8  
US-09-092-409-6  
Sequence 6, Application US/09092409  
Patent No. 6159478  
GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
ATTORNEY: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,409  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/680,726  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:





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; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,967
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-08-676-967-1

Query Match      38.7%; Score 41; DB 1; Length 759;
Best Local Similarity 47.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      2 GYAFVDCPDSEWALKAI 18
DB      541 GYAFAEQEHKAL 557

RESULT 13
US-08-676-974-1
; Sequence 1, Application US/08676974
; Patent No. 5770422
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,974
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-09-098-487-1

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; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-08-676-974-1

Query Match      38.7%; Score 41; DB 1; Length 759;
Best Local Similarity 47.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      2 GYAFVDCPDSEWALKAI 18
DB      541 GYAFAEQEHKAL 557

RESULT 14
US-09-098-487-1
; Sequence 1, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-09-098-487-1

Query Match      38.7%; Score 41; DB 2; Length 759;
Best Local Similarity 47.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      2 GYAFVDCPDSEWALKAI 18
DB      541 GYAFAEQEHKAL 557

RESULT 15
US-09-564-805-2
; Sequence 2, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:

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; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 826
; TYPE: ERT
; ORGANISM: Homo sapiens
US-09-564-805-2

Query Match          38.7%; Score 41; DB 4; Length 826;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 GYAF--VDCPDSEW 13
   | | | | |
Db 303 GAFAFVVECPDESF 316

Search completed: April 16, 2003, 16:22:58
Job time : 3.06076 secs
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GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:21:35 ; Search time 1.43514 Seconds

(without alignments)  
1001.062 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Sequence: 1 TGAFAVDCPDSWALKAIE 19

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Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database : Published Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	579	10	US-09-735-705-176 Sequence 176, App
2	106	100.0	579	10	US-09-735-705-348 Sequence 348, App
3	106	100.0	579	10	US-09-850-716A-176 Sequence 176, App
4	106	100.0	579	10	US-09-850-716A-348 Sequence 348, App
5	106	100.0	579	10	US-09-897-778-176 Sequence 176, App
6	106	100.0	579	10	US-09-897-778-348 Sequence 348, App
7	106	100.0	579	10	US-09-897-778-446 Sequence 446, App
8	106	100.0	579	10	US-09-897-778-446 Sequence 446, App
9	106	100.0	586	10	US-09-850-716A-427 Sequence 427, App
10	106	100.0	586	10	US-09-850-716A-427 Sequence 427, App
11	95	89.6	577	10	US-09-873-637-2 Sequence 2, Appli
12	93	87.7	18	10	US-09-897-778-465 Sequence 465, App
13	88	83.0	20	10	US-09-735-705-400 Sequence 400, App
14	88	83.0	20	10	US-09-850-716A-400 Sequence 400, App
15	88	83.0	20	10	US-09-897-778-400 Sequence 400, App
16	88	83.0	20	10	US-09-897-778-457 Sequence 457, App
17	80	75.5	20	10	US-09-735-705-399 Sequence 399, App
18	80	75.5	20	10	US-09-850-716A-399 Sequence 399, App
19	80	75.5	20	10	US-09-897-778-399 Sequence 399, App

20	80	75.5	620	10	US-09-764-864-1116 Sequence 1116, Ap
21	66	62.3	11	10	US-09-897-778-466 Sequence 466, App
22	48.5	45.8	303	9	US-09-925-299-851 Sequence 851, App
23	48.5	45.8	303	10	US-09-925-299-851 Sequence 851, App
24	44	41.5	359	9	US-10-025-367-25 Sequence 25, Appl
25	43	40.6	391	9	US-10-156-215-6 Sequence 6, Appli
26	43	40.6	578	10	US-09-925-300-1496 Sequence 1496, Ap
27	43	40.6	1179	10	US-09-821-883-29 Sequence 29, Appl
28	41.5	39.2	899	10	US-09-815-242-5356 Sequence 5356, Ap
29	41.5	39.2	932	10	US-09-815-242-12615 Sequence 12615, A
30	41	38.7	52	9	US-09-796-692-1087 Sequence 1087, Ap
31	41	38.7	52	9	US-09-796-692-1561 Sequence 1561, Ap
32	41	38.7	60	9	US-09-796-692-878 Sequence 878, App
33	41	38.7	68	9	US-09-796-692-887 Sequence 687, App
34	41	38.7	76	9	US-09-796-692-1076 Sequence 1076, Ap
35	41	38.7	82	9	US-09-796-692-1641 Sequence 1641, Ap
36	41	38.7	211	10	US-09-925-302-786 Sequence 786, App
37	41	38.7	521	10	US-09-925-300-1667 Sequence 1667, Ap
38	41	38.7	618	10	US-09-815-242-10864 Sequence 10864, A
39	41	38.7	690	10	US-09-768-877-28 Sequence 28, Appl
40	41	38.7	826	9	US-09-988-626-2 Sequence 2, Appli
41	41	38.7	826	9	US-09-988-626-224 Sequence 224, App
42	41	38.7	826	9	US-09-988-626-226 Sequence 226, App
43	41	38.7	826	9	US-09-988-687-2 Sequence 2, Appli
44	41	38.7	826	9	US-09-988-687-324 Sequence 224, App
45	41	38.7	826	9	US-09-988-687-226 Sequence 226, App

## ALIGNMENTS

RESULT 1\nUS-09-735-705-176\nSequence 176, Application US/09735705\nPatent No. US20020052329A1\nGENERAL INFORMATION:\nAPPLICANT: Wang, Tongtong\nAPPLICANT: Rao, Liqun\nAPPLICANT: Kato, Michael D.\nAPPLICANT: Bangur, Chaitanya S.\nAPPLICANT: Hosken, Nancy\nAPPLICANT: Fanger, Gary R.\nAPPLICANT: Li, Samuel X.\nAPPLICANT: Wang, Aijun\nAPPLICANT: Skeiky, Yasir A.W.\nAPPLICANT: Henderson, Robert A.\nAPPLICANT: McNeill, Patricia D.\nAPPLICANT: Fanger, Neil\nTITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY\nFILE REFERENCE: 210121.455C14\nCURRENT APPLICATION NUMBER: US/09/735,705\nCURRENT FILING DATE: 2000-12-12\nNUMBER OF SEQ ID NOS: 419\nSOFTWARE: FastSeq for Windows Version 3.0\nSEQ ID NO 176\nLENGTH: 579\nTYPE: PRT\nORGANISM: Homo sapiens\nUS-09-735-705-176\nQuery Match 100.0%; Score 106; DB 10; Length 579;\nBest Local Similarity 100.0%; Pred. No. 2e-08;\nMatches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;\nCy 1 TGAFAVDCPDSWALKAIE 19\nDb 37 TGAFAVDCPDSWALKAIE 55\nRESULT 2\nUS-09-735-705-348\nSequence 348, Application US/09735705

```
Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Ligu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Seikly, Jasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-348

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 3
US-09-850-716A-176
; Sequence 176, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 4
US-09-850-716A-348
; Sequence 348, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
```

```
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-348

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 5
US-09-897-778-176
; Sequence 176, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-176

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 6
US-09-897-778-348
; Sequence 348, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 7
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 8
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

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; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55

RESULT 9
US-09-850-716A-427
; Sequence 427, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-427

Query Match          100.0%; Score 106; DB 10; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDDESMALKATE 19
DB 44 TGYAFVDCPDDESMALKATE 62

RESULT 10
US-09-897-778-427
; Sequence 427, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 427
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Page 4

LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-427

Query Match 100.0%; Score 106; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
DB 44 TGYAFVDCPDESMALKAIE 62

RESULT 11  
US-09-873-637-2  
Sequence 2, Application US/09873637  
Patent No. US20020061543A1  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/873.637  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-873-637-2

Query Match 89.6%; Score 95; DB 10; Length 577;  
Best Local Similarity 84.2%; Pred. No. 9.4e-07;  
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
DB 37 SGYAFVDCPDESMALKAIE 55

RESULT 12  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Mannerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darlick  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897.778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 465  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-465

Query Match 87.7%; Score 93; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALK 16  
DB 1 TGYAFVDCPDESMALK 16

RESULT 13  
US-09-735-705-400  
Sequence 400, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735.705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-400

Query Match 83.0%; Score 88; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPDESMALKAIE 19  
DB 1 AFVDCPDESMALKAIE 16

RESULT 14  
US-09-850-716A-400  
Sequence 400, Application US/09850716A  
Patent No. US20020115139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850.716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match 83.0%; Score 88; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPDESMALKAIE 19  
DB 1 AFVDCPDESMALKAIE 16

us-09-897-778-176\_copy\_37\_55.rabb

Page 5

	Query Match	83.0%	Score 88:	DB 10:	length 20;
	Best Local Similarity	100.0%:	Pred. No.	3.9e-07:	
	Matches	16;	Conservative	0;	Mismatches 0; Indels 0;
Oy	4 AFVDCPDSESMALKATE	19			
Db	1 AFVDCPDSESMALKATE	16			

Search completed: April 16, 2003, 16:32:08  
Job time : 3.43514 secs









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APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrik
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Beckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45503PC
CURRENT FILING DATE: 2001-11-30
CURRENT APPLICATION NUMBER: PCT/US01/47576
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 449
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-47576-449
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Query Match          100.0%; Score 106; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 TGYAFVDCPDESMALKATE 19
    |||||
Db 37 TGYAFVDCPDESMALKATE 55
```

```
RESULT 6
US-09-466-396A-176
; Sequence 176, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.45504
; CURRENT FILING DATE: 1999-12-17
; CURRENT APPLICATION NUMBER: US/09/466,396A
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-396A-176
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```
Query Match          100.0%; Score 106; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 TGYAFVDCPDESMALKATE 19
    |||||
Db 37 TGYAFVDCPDESMALKATE 55
```

```
RESULT 7
US-09-476-496A-176
; Sequence 176, Application US/09476496A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
```

```
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
FILE REFERENCE: 210121.45505
CURRENT APPLICATION NUMBER: US/09/476,496A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-476-496A-176
```

```
Query Match          100.0%; Score 106; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDESMALKATE 19
    |||||
Db 37 TGYAFVDCPDESMALKATE 55
```

```
RESULT 8
US-09-480-884A-176
; Sequence 176, Application US/09480884A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45506
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-884A-176
```

```
Query Match          100.0%; Score 106; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDESMALKATE 19
    |||||
Db 37 TGYAFVDCPDESMALKATE 55
```

```
RESULT 9
US-09-510-376A-176
; Sequence 176, Application US/09510376A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45507
; CURRENT APPLICATION NUMBER: US/09/510,376A
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-510-376A-176

Query Match 100.0%; Score 106; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19  
DB 37 TGYAFVDCPDSEWALKATE 55

RESULT 10  
US-09-542-615A-176  
Sequence 176, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542,615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-542-615A-176

Query Match 100.0%; Score 106; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19  
DB 37 TGYAFVDCPDSEWALKATE 55

RESULT 11

US-09-542-615A-348  
Sequence 348, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542,615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-542-615A-348

Query Match 100.0%; Score 106; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19  
DB 37 TGYAFVDCPDSEWALKATE 55

RESULT 12  
US-09-606-421A-176  
Sequence 176, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-606-421A-176

Query Match 100.0%; Score 106; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19  
DB 37 TGYAFVDCPDSEWALKATE 55

RESULT 13  
US-09-606-421A-348  
Sequence 348, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-606-421A-348

Query Match 100.0%; Score 106; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19  
DB 37 TGYAFVDCPDSEWALKATE 55

RESULT 14





GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:19:55 ; Search time 2.3399 Seconds  
(without alignments)  
1266.170 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 106  
Sequence: 1 TGYAFVDCPDESMALKAIE 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 705215 seqs, 155932251 residues

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/paa/US08\_NEW.COMB.pep.\*  
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7: /cgn2\_6/ptodata/1/paa/US60\_NEW.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	43	US-10-313-986-482	Sequence 482, App
2	106	100.0	134	US-09-724-676-92917	Sequence 92917, A
3	106	100.0	134	US-09-724-676A-92917	Sequence 92917, A
4	106	100.0	492	US-09-724-676-92916	Sequence 92916, A
5	106	100.0	492	US-09-724-676A-92916	Sequence 92916, A
6	106	100.0	558	US-09-724-676-92918	Sequence 92918, A
7	106	100.0	558	US-09-724-676A-92918	Sequence 92918, A
8	106	100.0	579	US-10-313-986-176	Sequence 176, App
9	106	100.0	579	US-10-313-986-348	Sequence 348, App
10	106	100.0	579	US-10-313-986-446	Sequence 446, App
11	106	100.0	579	US-10-313-986-449	Sequence 449, App
12	106	100.0	579	US-10-313-986-480	Sequence 480, App
13	106	100.0	579	US-10-313-986-484	Sequence 484, App
14	106	100.0	579	US-10-313-986-485	Sequence 485, App
15	106	100.0	586	US-10-313-986-427	Sequence 427, App
16	106	100.0	586	US-10-313-986-486	Sequence 486, App
17	95	89.6	572	US-09-724-676-48617	Sequence 48617, A
18	95	89.6	572	US-09-724-676A-48617	Sequence 48617, A
19	95	89.6	572	US-09-724-676-48618	Sequence 48618, A
20	95	89.6	572	US-09-724-676A-48618	Sequence 48618, A
21	95	89.6	577	US-09-724-676-48616	Sequence 48616, A
22	95	89.6	598	US-09-724-676-48621	Sequence 48621, A
23	95	89.6	598	US-09-724-676A-48621	Sequence 48621, A
24	95	89.6	598	US-09-724-676-48619	Sequence 48619, A
25	95	89.6	602	US-09-724-676A-48619	Sequence 48619, A
26	95	89.6	602	US-09-724-676-48619	Sequence 48619, A

27	95	89.6	602	US-09-724-676-48620	Sequence 48620, A
28	95	89.6	602	US-09-724-676A-48619	Sequence 48619, A
29	95	89.6	602	US-09-724-676A-48620	Sequence 48620, A
30	93	87.7	18	US-10-313-986-465	Sequence 465, App
31	88	83.0	20	US-10-313-986-400	Sequence 400, App
32	88	83.0	20	US-10-313-986-457	Sequence 457, App
33	88	83.0	20	US-10-313-986-508	Sequence 508, App
34	80	75.5	20	US-10-313-986-399	Sequence 399, App
35	80	75.5	20	US-10-313-986-470	Sequence 470, App
36	80	75.5	20	US-10-313-986-507	Sequence 507, App
37	80	75.5	20	US-09-513-999C-7342	Sequence 7342, App
38	80	75.5	556	US-60-453-135-11528	Sequence 11528, A
39	80	75.5	556	US-60-453-135-11528	Sequence 11528, A
40	80	75.5	587	US-60-453-135-11527	Sequence 11527, A
41	80	75.5	587	US-60-453-135-11527	Sequence 11527, A
42	80	75.5	599	US-60-453-050-11527	Sequence 11527, A
43	69	65.1	255	US-60-452-680-15601	Sequence 15601, A
44	69	65.1	555	PCT-US02-31357-40	Sequence 40, Appl
45	69	65.1	555	US-10-262-445-40	Sequence 40, Appl

## ALIGNMENTS

RESULT 1  
US-10-313-986-482  
Sequence 482, Application US/10313986  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria  
APPLICANT: Matanabe, Yoshinori  
APPLICANT: Reed, Steven G.  
APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C19  
CURRENT APPLICATION NUMBER: US/10/313,986  
NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 482  
LENGTH: 43  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-482

Query Match 100.0%; Score 106; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGYAFVDCPDESMALKAIE 19  
Db 5 TGYAFVDCPDESMALKAIE 23  
RESULT 2  
US-09-724-676-92917  
Sequence 92917, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92917  
Query Match 100.0%; Score 106; DB 5; Length 134;

Thu Apr 17 07:55:19 2003

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Page 2

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Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 3
US-09-724-676A-92917
; Sequence 92917, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92917

Query Match 100.0%; Score 106; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 4
US-09-724-676-92916
; Sequence 92916, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92916

Query Match 100.0%; Score 106; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 5
US-09-724-676A-92916
; Sequence 92916, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92916

Query Match 100.0%; Score 106; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 6
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match 100.0%; Score 106; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 7
US-09-724-676A-92918
; Sequence 92918, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92918

Query Match 100.0%; Score 106; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 8
US-10-313-986-176
; Sequence 176, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
```



```

; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

```

```

Query Match      100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGYAFVDCPDSESMALKATE 19
    |||
Db 37 TGYAFVDCPDSESMALKATE 55

```

```

RESULT 9
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

```

```

Query Match      100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGYAFVDCPDSESMALKATE 19
    |||
Db 37 TGYAFVDCPDSESMALKATE 55

```

```

RESULT 10
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-10-313-986-446

```

```

Query Match      100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGYAFVDCPDSESMALKATE 19
    |||
Db 37 TGYAFVDCPDSESMALKATE 55

```

```

RESULT 11
; Sequence 449, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-449

```

```

Query Match      100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGYAFVDCPDSESMALKATE 19
    |||
Db 37 TGYAFVDCPDSESMALKATE 55

```

```

RESULT 12
; Sequence 480, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-480

```

```

Query Match      100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGYAFVDCPDSESMALKATE 19
    |||
Db 37 TGYAFVDCPDSESMALKATE 55

```

```
RESULT 13
US-10-313-986-484
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 484
; LENGTH: 579
; TYPE: PRT
; ORGANISM: primate
US-10-313-986-484

Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAFVDCPDPSWALKATE 19
Db 37 TGAFVDCPDPSWALKATE 55

RESULT 14
US-10-348-119-255
; Sequence 255, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348.119
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 255
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-119-255

Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAFVDCPDPSWALKATE 19
Db 37 TGAFVDCPDPSWALKATE 55

RESULT 15
US-10-313-986-427
; Sequence 427, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-427

Query Match          100.0%; Score 106; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAFVDCPDPSWALKATE 19
Db 44 TGAFVDCPDPSWALKATE 62

Search completed: April 16, 2003, 16:31:15
Job time : 3.339 secs
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GenCore version 5.1.4.P5-4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:22:25 ; Search time 2.52874 Seconds  
(without alignments)  
579.640 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51  
Perfect score: 11  
Sequence: 1 FVDCPDESWAL 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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3: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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21: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID52/gcgcdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	23	ABR75070
2	11	100.0	18	23	ABR75069
3	11	100.0	20	23	ABR75027
4	11	100.0	20	23	ABR75061
5	11	100.0	20	23	ABR75061
6	11	100.0	579	21	ABR11328
7	11	100.0	579	21	ABR74960
8	11	100.0	579	23	ABR74997
9	11	100.0	579	23	ABR75053
10	11	100.0	579	23	ABR75054

11	11	100.0	586	23	ABR75048	Human lung tumour
12	11	100.0	619	22	ABG21963	Novel human diagno
13	9	81.8	20	23	ABR75026	Human lung tumour
14	7	63.6	209	22	ABG21961	Novel human diagno
15	7	63.6	266	22	ABG12593	Novel human diagno
16	7	63.6	577	20	AAV30649	A murine c-myc cod
17	7	63.6	583	22	ABG12592	Novel human diagno
18	5	45.5	49	15	AAH49438	Murine HLA-DRAp
19	5	45.5	49	15	AAH49589	Sequence of HLA-DR
20	5	45.5	52	23	ABP02466	Human OREF protein
21	5	45.5	53	23	ABP01689	Human OREF protein
22	5	45.5	54	23	ABP33654	Human OREF267 prot
23	5	45.5	63	20	AAV41340	Human secreted pro
24	5	45.5	71	22	ABG31221	Peptide #3872 enco
25	5	45.5	71	22	ABG36428	Peptide #3934 enco
26	5	45.5	71	22	ABR21780	Protein #3779 enco
27	5	45.5	71	22	AAH57186	Human brain expres
28	5	45.5	71	22	AAH65991	Human bone marrow
29	5	45.5	71	22	AAH17405	Peptide #3839 enco
30	5	45.5	71	22	AAH29927	Peptide #3964 enco
31	5	45.5	71	22	AAH05090	Peptide #3772 enco
32	5	45.5	93	23	ABG39212	Human peptide enco
33	5	45.5	93	23	ABP06400	Human OREF protein
34	5	45.5	94	22	ABR87388	Human gene 47 enco
35	5	45.5	94	23	ABG65366	Human albumin fusi
36	5	45.5	109	22	AAH29896	Novel human secret
37	5	45.5	122	22	AAU42819	Protonbacterium
38	5	45.5	135	23	ABP03056	Human OREF protein
39	5	45.5	144	22	AAH58517	Protonbacterium
40	5	45.5	150	21	AAH56957	Human prostate can
41	5	45.5	150	23	AAE22108	Human 48921 quantin
42	5	45.5	155	21	AAH01801	Rice M10 homologue
43	5	45.5	174	21	ABH41067	Human OREF ORF31
44	5	45.5	174	21	ABH41067	Human OREF protein
45	5	45.5	196	22	ABG02217	Novel human diagno

#### ALIGNMENTS

```
RESULT 1
ABR75070
ID ABR75070 standard; Peptide: 11 AA.
XX
AC ABR75070;
XX
DT 01-MAY-2002 (first entry)
XX
DE L523S antigenic epitope seq ID NO:466.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW Immune response.
XX
OS Homo sapiens.
XX
PN WO200200174-A2.
XX
PD 03-JAN-2002.
XX
PE 28-JUN-2001; 2001WO-US21065.
XX
PF 28-JUN-2000; 2000US-0606421.
XX
PR 02-AUG-2000; 2000US-0630940.
XX
PR 21-AUG-2000; 2000US-0643597.
XX
PR 15-SEP-2000; 2000US-0662786.
XX
PR 09-OCT-2000; 2000US-0685696.
XX
PR 12-DEC-2000; 2000US-0735705.
XX
PR 07-MAY-2001; 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
McNeill PD, Fanger N, Retter MW, Manterakis M, Fanger GR;
```

PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
XX  
XX WPI: 2002-090513/12.  
DR N-PSDB: ABL49300.  
XX  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Claim 2: Page 168; 374pp; English.  
XX  
XX The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production, compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to  
CC ABB75070 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 11 AA:  
Query Match 100.0%; Score 11; DB 23; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.7e-07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVDCPDESWMAL 11  
DB 1 FVDCPDESWMAL 11  
RESULT 2  
ID ABB75069  
XX ABB75069 standard; Peptide; 18 AA.  
XX  
AC ABB75069;  
XX  
XX 01-MAY-2002 (first entry)  
XX  
XX Human lung tumour L523S epitope SEQ ID NO:465.  
XX  
XX Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
KW immune response.  
XX  
XX Homo sapiens.  
OS  
XX WO200200174-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 28-JUN-2001; 2001WO-US21065.  
XX  
XX 28-JUN-2000; 2000US-0606421.  
PR 02-AUG-2000; 2000US-0630940.  
PR 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
PR 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
PR 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
PI McNeill PD, Fanger N, Reiter MW, Marnerakis M, Fanger GR;  
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
XX  
XX WPI: 2002-090513/12.  
XX  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Claim 2: Page 168; 374pp; English.

CC The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production, compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to  
CC ABB75070 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 18 AA:  
Query Match 100.0%; Score 11; DB 23; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.0e-07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVDCPDESWMAL 11  
DB 5 FVDCPDESWMAL 15  
RESULT 3  
ID ABB75027  
XX ABB75027 standard; Peptide; 20 AA.  
XX  
XX ABB75027;  
XX  
XX 01-MAY-2002 (first entry)  
XX  
XX Human lung tumour L523S peptide SEQ ID NO:400.  
XX  
XX Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
KW immune response.  
XX  
XX Homo sapiens.  
OS  
XX WO200200174-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 28-JUN-2001; 2001WO-US21065.  
XX  
XX 28-JUN-2000; 2000US-0606421.  
PR 02-AUG-2000; 2000US-0630940.  
PR 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
PR 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
PR 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
PI McNeill PD, Fanger N, Reiter MW, Marnerakis M, Fanger GR;  
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
XX  
XX WPI: 2002-090513/12.  
XX  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Claim 2: Page 348; 374pp; English.

SQ Sequence 20 AA;

Query Match 100.0%; Score 11; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESMAL 11  
 |||||  
 Db 2 FVDCPDSESMAL 12

## RESULT 4

ABB75061  
 ID ABB75061 standard; Peptide; 20 AA.

AC ABB75061;

XX 01-MAY-2002 (first entry)

DE Human lung tumour L5235 epitope SEQ ID NO:457.

XX Human lung tumour; Lung cancer; cytostatic; immunostimulant; vaccine;

KW immune response.

XX Homo sapiens.

OS WO200200174-A2.

PN 03-JAN-2002.

PD 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skelky YAN, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

DR Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Claim 2: Page 167; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

CC ABB75070 represent sequences used in the exemplification of the present

CC invention.

## RESULT 5

AAB11328

ID AAB11328 standard; Protein; 579 AA.

XX AAB11328;

XX 21-FEB-2001 (first entry)

DE Human lung cancer-associated protein L5235.

XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

KW vaccine; detection.

XX Homo sapiens.

OS WO200061612-A2.

PN 19-OCT-2000.

PD 03-APR-2000; 2000WO-US08896.

XX 02-APR-1999; 99US-0285479.

XX 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

DR N-PSDB; AAC65900.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor

PT protein is used for detecting and monitoring progression of a lung cancer

XX in a patient -

XX Claim 3: Page 186-188; 261pp; English.

XX This invention describes a novel isolated polypeptide (1) which

CC comprising an immunogenic portion of a lung tumor protein or variant (P2)

CC which have cytostatic activity. The polypeptides and polynucleotides are

CC used in compositions and vaccines to inhibit the development of cancer,

CC especially lung cancer, in a patient. Methods described in the invention

CC can be used to monitor the progression of a cancer by carrying out the

CC detection at subsequent time points and comparing the results from the

CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient

CC are treated with P2, polynucleotides encoding P2 or antigen presenting

CC cells expressing P2 and then administered to the patient to inhibit

CC development of cancer.

SQ Sequence 579 AA;

Query Match 100.0%; Score 11; DB 21; Length 579;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESMAL 11  
 |||||  
 Db 41 FVDCPDSESMAL 51

## RESULT 6

AAB11365

ID AAB11365 standard; Protein; 579 AA.

XX AAB11365;

XX 21-FEB-2001 (first entry)

DE Human lung cancer associated antigen L5235.



XX (CORI-) CORIXA CORP.  
PA Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
XX McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
PI Veevick TS, Carter D, Watanabe Y, Peckham DW;  
XX WPI: 2002-090513/12.  
DR N-PSDB; ABL49254.  
XX  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Example 2; Page 330-332; 374pp; English.  
XX  
XX The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to  
CC ABL75070 represent sequences used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 579 AA;  
SO  
Query Match 100.0%; Score 11; DB 23; Length 579;  
Best Local Similarity 100.0%; Pred. NO. 1.6e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FVDCPDESMA 11  
DB 41 FVDCPDESMA 51  
RESULT 9  
ID ABL75053  
AB 75053 standard; Protein; 579 AA.  
XX  
AC ABB75053;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human lung tumour L523S recombinant protein sequence SEQ ID NO:446.  
XX  
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
KW immune response.  
XX  
OS Homo sapiens.  
XX  
PN W0200200174-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 28-JUN-2001; 2001WO-US21065.  
XX  
PR 28-JUN-2000; 2000US-0606421.  
PR 02-AUG-2000; 2000US-0630940.  
PR 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
PR 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
PR 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
PI Veevick TS, Carter D, Watanabe Y, Peckham DW;  
XX  
XX WPI: 2002-090513/12.  
DR N-PSDB; ABL49297.  
DR

XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Claim 2; Page 365-367; 374pp; English.  
XX  
XX The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to  
CC ABL75070 represent sequences used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 579 AA;  
SO  
Query Match 100.0%; Score 11; DB 23; Length 579;  
Best Local Similarity 100.0%; Pred. NO. 1.6e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FVDCPDESMA 11  
DB 41 FVDCPDESMA 51  
RESULT 10  
ID ABL75054  
AB 75054 standard; Protein; 579 AA.  
XX  
AC ABB75054;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human lung tumour L523S recombinant protein sequence SEQ ID NO:449.  
XX  
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
KW immune response.  
XX  
OS Homo sapiens.  
XX  
PN W0200200174-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 28-JUN-2001; 2001WO-US21065.  
XX  
PR 28-JUN-2000; 2000US-0606421.  
PR 02-AUG-2000; 2000US-0630940.  
PR 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
PR 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
PR 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
PI Veevick TS, Carter D, Watanabe Y, Peckham DW;  
XX  
XX WPI: 2002-090513/12.  
DR N-PSDB; ABL49299.  
DR  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Claim 2; Page 368-369; 374pp; English.  
XX  
XX The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions

Query Match	Best Local Similarity	Score 11: 100.0%	DB 23: 100.0%	Length 579:
Matches 11: Conservative	0: Mismatches	0: Indels	0: Gaps	0
SO	Sequence	579 AA:		
CC	compiling the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present invention.			
XX				
YY	1 FVDCDESMAL 11			
DB	41 FVDCDESMAL 51			
RESULT 11				
ABB75048				
ID	ABB75048 standard; Protein: 586 AA.			
AC	ABB75048;			
XX				
DT	01-MAY-2002 (first entry)			
XX				
DE	Human lung tumour L5235 recombinant protein sequence SEQ ID NO:427.			
XX				
KW	Human: lung tumour; lung cancer; cytosolic; immunostimulant; vaccine; immune response.			
XX				
OS	Homo sapiens.			
XX				
PN	WC0200200174-A2.			
PD	03-JAN-2002.			
XX				
PF	28-JUN-2001: 2001WO-0521065.			
XX				
PR	28-JUN-2000: 2000US-0606421.			
PR	02-AUG-2000: 2000US-0630940.			
PR	21-AUG-2000: 2000US-0643597.			
PR	15-SEP-2000: 2000US-0662786.			
PR	09-OCT-2000: 2000US-0685696.			
PR	12-DEC-2000: 2000US-0735705.			
PR	07-MAY-2001: 2001US-0850716.			
XX				
PA	(CORI-) CORIXA CORP.			
PI	Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;			
PI	McNeill PD, Fanger N, Reltier MW, Marnettakis M, Fanger GR;			
PI	Vedvick TS, Carter D, Watanabe Y, Peckham DW;			
XX				
DR	WPI: 2002-090513/12.			
DR	N-PDB: ABL49283.			
XX				
PT	Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -			
XX				
PS	Claim 2: Page 354-355; 374pp; English.			
CC	The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present invention.			
CC				
XX	Sequence	586 AA:		

Query	Match	Similarity	100.0%	Score 11	DB 23	Length 586		
Matches	11	Conservative	0	Mismatches	0	Indels	Gaps	0
QY	1	FVCCPQESNAL	11					
DB	48	FVDCPQESNAL	58					
RESULT 12								
ID	ABG21963	standard; Protein; 619 AA.						
AC	ABG21963							
DT	18-FEB-2002	(first entry)						
DE	Novel human diagnostic protein #21954.							
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.							
OS	Homo sapiens.							
SN	WO200175067-A2.							
PN								
FD	11-OCT-2001.							
PE	30-MAR-2001; 2001WO-US08631.							
PR	31-MAR-2000; 2000US-0540217.							
PR	23-AUG-2000; 2000US-0649167.							
PA	(HYSE-) HYSEQ INC.							
XX								
PT	Dymanac RT, Liu C, Tang YT;							
DR	WPI; 2001-639362/73.							
DR	N-PSDB; AAS86150.							
XX								
PT	New isolated polynucleotide and encoded polypeptides, useful in							
PT	diagnostics, forensics, gene mapping, identification of mutations							
PT	responsible for genetic disorders or other traits and to assess							
PT	biodiversity -							
XX								
PS	Claim 20; SEQ ID No 52322; 103bp; English.							
XX								
CC	The invention relates to isolated polynucleotide (I) and							
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,							
CC	polynucleotide chain reaction (PCR) primers, oligomers, and for chromosome							
CC	and gene mapping, and in recombinant production of (II). The							
CC	polynucleotides are also used in diagnostics as expressed sequence tags							
CC	for identifying expressed genes. (I) is useful in gene therapy techniques							
CC	to restore normal activity of (II) or to treat disease states involving							
CC	(II). (II) is useful for generating antibodies against it, detecting or							
CC	quantitating a polypeptide in tissue, as molecular weight markers and as							
CC	a food supplement. (II) and its binding partners are useful in medical							
CC	imaging of sites expressing (II). (I) and (II) are useful for treating							
CC	disorders involving aberrant protein expression or biological activity.							
CC	The polypeptide and polynucleotide sequences have applications in							
CC	diagnostics, forensics, gene mapping, identification of mutations							
CC	responsible for genetic disorders or other traits to assess biodiversity							
CC	and to produce other types of data and products dependent on DNA and							
CC	amino acid sequences. AbG00010-ABG30377 represent novel human							
CC	diagnostic amino acid sequences of the invention.							
CC	Note: The sequence data for this patent did not appear in the printed							
CC	specification, but was obtained in electronic format directly from WIPO							
CC	at <a href="http://wipo.int/pub/Published_pcl_sequences">http://wipo.int/pub/Published_pcl_sequences</a> .							
XX								
XX	Sequence 619 AA:							

Query Match	100.0%;	Score 11;	DB 22;	Length 619;
Best Local Similarity	100.0%;	Pred. No. 1.7e-05;		



Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 FVDCPDSESMAL 11  
 |||||||  
 DB 77 FVDCPDSESMAL 87

## RESULT 13

ABR75026  
 ID ABR75026 standard; Peptide: 20 AA.

AC ABR75026;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L5235 peptide SEQ ID NO:399.

KM Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX immune response.

OS Homo sapiens.

PN WO200200174-A2.

PD 03-JAN-2002.

PF 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Ranger N, Rector MW, Marneakis M, Ranger GR;

PI Vevick TS, Carter D, Watanabe Y, Peckham DW;

DR WPI: 2002-090513/12.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Claim 2; Page 348; 374pp: English.

CC The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to

CC ABR75070 represent sequences used in the exemplification of the present

CC invention.

XX Sequence 20 AA;

SO Query Match

Best Local Similarity 81.8%; Score 9; DB 23; Length 20;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESM 9

|||

DB 12 FVDCPDSESM 20

RESULT 14

ABG21961

ID ABG21961 standard; Protein: 209 AA.

XX ABR75026;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #21952.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YF;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS86148.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 20; SEQ ID NO 52320; 103pp: English.

CC The invention relates to isolated polynucleotide (I) and

CC polynucleotide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABR00010-ABG30377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at [http://wipo.int/pub/published\\_pcl\\_sequences](http://wipo.int/pub/published_pcl_sequences).

XX Sequence 209 AA;

SO Query Match

Best Local Similarity 63.6%; Score 7; DB 22; Length 209;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDE 7

|||

DB 18 FVDCPDE 24

RESULT 15

ABG12593

ID ABG12593 standard; Protein: 266 AA.

AC ABG12593;

XX 18-FEB-2002 (first entry)  
DT  
XX Novel human diagnostic protein #12584.  
DE  
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001MO-US08631.  
XX  
XX 31-MAR-2000; 2000US-0540217.  
XX  
XX 23-AUG-2000; 2000US-0649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI: 2001-639362/73.  
XX  
XX N-PSDB; AAS76780.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
XX Claim 20; SEQ ID No 42952; 103bp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against, detecting or  
XX identifying polypeptides in tissues, as molecular weight standards as  
XX a food supplement, or in assessing its binding. (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. Abg00010-Abg30377 represent novel human  
XX diagnostic amino acid sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
XX Sequence 266 AA:  
SQ

Query Match 63.6%; Score 7; DB 22; Length 266;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FVDCPDE 7  
|||||  
Db 21 FVDCPDE 27

Search completed: April 16, 2003, 16:34:38  
Job time: 4.52874 secs

GenCore version 5.1.4.P5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:32:15 ; Search time 0.776683 Seconds  
(without alignments)  
416.711 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Sequence: 1 FVDCPDESMAL 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PCUUS.COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	11	100.0	579	US-09-643-597-176	Sequence 176, App
2	11	100.0	579	US-09-643-597-348	Sequence 348, App
3	7	63.6	577	US-09-261-855-2	Sequence 2, Appli
4	5	45.5	294	US-08-973-334-2	Sequence 2, Appli
5	5	45.5	294	US-09-563-869A-2	Sequence 2, Appli
6	5	45.5	294	US-08-548-489-2	Sequence 2, Appli
7	5	45.5	309	US-09-109-205-1	Sequence 1, Appli
8	5	45.5	325	US-09-088-435-1	Sequence 1, Appli
9	5	45.5	534	US-08-875-223-8	Sequence 8, Appli
10	5	45.5	826	US-09-564-805-2	Sequence 2, Appli
11	5	45.5	826	US-09-564-805-224	Sequence 224, App
12	5	45.5	826	US-09-564-805-226	Sequence 226, App
13	5	45.5	1059	US-09-134-513-2	Sequence 2, Appli
14	5	45.5	1070	US-08-633-770A-2	Sequence 3, Appli
15	5	45.5	1255	US-08-947-823-3	Sequence 3, Appli
16	5	45.5	1257	US-08-947-823-5	Sequence 5, Appli
17	5	45.5	1529	US-09-134-001C-945	Sequence 3945, Ap
18	5	45.5	1956	US-08-843-417-2	Sequence 2, Appli
19	5	45.5	1957	US-08-669-656A-2	Sequence 8, Appli
20	5	45.5	1957	US-08-669-656A-8	Sequence 2, Appli
21	5	45.5	2132	US-08-669-656A-6	Sequence 6, Appli
22	4	36.4	4	US-08-478-386A-7	Sequence 7, Appli
23	4	36.4	4	US-08-292-597-7	Sequence 7, Appli
24	4	36.4	4	US-08-388-653-7	Sequence 7, Appli
25	4	36.4	4	US-08-473-985-7	Sequence 7, Appli
26	4	36.4	4	US-08-483-898-7	Sequence 7, Appli
27	4	36.4	4	US-09-087-716-7	Sequence 7, Appli

28	4	36.4	4	US-09-157-753-7	Sequence 7, Appli
29	4	36.4	4	US-09-157-230-7	Sequence 7, Appli
30	4	36.4	4	US-09-087-811-7	Sequence 7, Appli
31	4	36.4	4	US-09-156-855-7	Sequence 7, Appli
32	4	36.4	4	US-09-158-010-7	Sequence 7, Appli
33	4	36.4	4	US-09-087-647-7	Sequence 7, Appli
34	4	36.4	4	US-09-302-629-7	Sequence 7, Appli
35	4	36.4	6	PCT-US94-01321-59	Sequence 59, Appli
36	4	36.4	6	PCT-US94-01321-60	Sequence 60, Appli
37	4	36.4	10	US-08-726-464B-8	Sequence 8, Appli
38	4	36.4	10	US-08-726-464B-11	Sequence 11, Appli
39	4	36.4	10	US-08-849-480A-19	Sequence 19, Appli
40	4	36.4	11	US-09-183-217-9	Sequence 9, Appli
41	4	36.4	16	US-08-769-745-27	Sequence 27, Appli
42	4	36.4	17	US-08-179-481-69	Sequence 69, Appli
43	4	36.4	17	US-08-743-200-4	Sequence 4, Appli
44	4	36.4	17	US-08-743-200-4	Sequence 4, Appli
45	4	36.4	19	US-08-789-333F-20	Sequence 20, Appli

## ALIGNMENTS

```

RESULT 1
US-09-643-597-176
: Sequence 176, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-643-597-176

Query Match      100.0%; Score 11; DB 4; Length 579;
Best local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY      1 FVDCPDESMAL 11
Db      41 FVDCPDESMAL 51

RESULT 2
US-09-643-597-348
: Sequence 348, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.

```

APPLICANT: Wang, Aijun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-348

Query Match 100.0%; Score 11; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPESMAL 11  
Db 41 FVDCPESMAL 51

RESULT 3  
US-09-261-855-2  
Sequence 2, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261,855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-2

Query Match 63.6%; Score 7; DB 4; Length 577;  
Best Local Similarity 100.0%; Pred. No. 0.84;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDE 7  
Db 41 FVDCPDE 47

RESULT 4  
US-08-973-334-2  
Sequence 2, Application US/08973334  
Patent No. 6261551  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Gao, Guang-Ping  
TITLE OF INVENTION: Recombinant Adenovirus and Adeno-  
TITLE OF INVENTION: Associated Virus, Cell Lines, and  
TITLE OF INVENTION: Methods of Production and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 No. 626151Irlstown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA

ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.0 Version 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,334  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/462,014  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/549,489  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNP/PN012C1PUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-973-334-2

Query Match 45.5%; Score 5; DB 4; Length 294;  
Best Local Similarity 100.0%; Pred. No. .86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ESMAL 11  
Db 118 ESMAL 122

RESULT 5  
US-09-563-869A-2  
Sequence 2, Application US/09563869A  
Patent No. 6270996  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Gao, Guang-Ping  
TITLE OF INVENTION: Recombinant Adenovirus and Adeno-  
TITLE OF INVENTION: Associated Virus, Cell Lines, and  
TITLE OF INVENTION: Methods of Production and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 No. 6270996Irlstown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.0 Version 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/563,869A  
FILING DATE: 03-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/973,334  
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/549,489  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNP/NO12CIPUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-563-869A-2

Query Match 45.5%; Score 5; DB 4; Length 294;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ESMAL 11  
Db 118 ESMAL 122

RESULT 6  
US-08-549-489-2  
Sequence 2, Application US/08549489  
Patent No. 6281010  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Gao, Guang-Ping  
TITLE OF INVENTION: No. 6281010e1 Adenovirus Gene Therapy Vehicle  
TITLE OF INVENTION: and Cell Line  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 No. 6281010Istown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/549,489  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/462,014  
FILING DATE: 08-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNP/NO13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-549-489-2

Query Match 45.5%; Score 5; DB 4; Length 294;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 7 ESMAL 11  
Db 118 ESMAL 122

RESULT 7  
US-09-109-205-1  
Sequence 1, Application US/09109205  
Patent No. 6057140  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Guegler, Karl J.  
APPLICANT: Gorgone, Gina  
APPLICANT: Corley, Neil C.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,205  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cetrone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0542 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT14  
CLONE: 1511003  
US-09-109-205-1

Query Match 45.5%; Score 5; DB 3; Length 309;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 3 DCPDE 7  
Db 136 DCPDE 140

RESULT 8  
US-09-088-435-1  
Sequence 1, Application US/09088435  
Patent No. 6277619

## GENERAL INFORMATION:

APPLICANT: LAL, PREETI  
APPLICANT: CORLEY, NEIL C.  
APPLICANT: GUEGLER, KARL J.  
APPLICANT: PATTERSON, CHANDRA  
TITLE OF INVENTION: SERINE DEHYDRATASE HOMOLOG  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088.435

## FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

## FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Carrone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0512 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: TPI1A2S08  
CLONE: 2752518

## US-09-088-435-1

Query Match 45.5%; Score 5; DB 4; Length 325;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESMAL 11  
Db 22 ESMAL 26

## RESULT 9

US-08-875-223-8  
Sequence 8, Application US/08875223  
Patent No. 6127175

## GENERAL INFORMATION:

APPLICANT: VIGNE, Emmanuelle  
APPLICANT: PERRICAUDET, Michel  
APPLICANT: DEDIEU, Jean-Francois  
APPLICANT: ORSINI, Cecile  
APPLICANT: YEH, Patricia  
APPLICANT: LATTA, Martine  
APPLICANT: PROST, Edouard  
TITLE OF INVENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT  
TITLE OF INVENTION: ADENOVIRUSES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcoia Road, Mailstop 3043  
CITY: Collegeville

## STATE: PA

COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,223  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/00747  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/06532  
FILING DATE: 01-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/10541  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR WO FR96/00088  
FILING DATE: 19-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehner Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95005G1-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-08-875-223-8

Query Match 45.5%; Score 5; DB 3; Length 534;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESMAL 11  
Db 358 ESMAL 362

## RESULT 10

US-09-564-805-2  
Sequence 2, Application US/09564805  
Patent No. 633403

## GENERAL INFORMATION:

APPLICANT: Tavligian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility  
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: 09/434,382  
PRIOR FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 826  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-564-805-2

Query Match 45.5%; Score 5; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CPDES 8  
DB 311 CPDES 315

RESULT 11  
US-09-564-805-224  
Sequence 224, Application US/09564805  
Patent No. 6333403  
GENERAL INFORMATION:  
APPLICANT: Tavligian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Myriad Genetics, Inc.  
TITLE OF INVENTION: Chromosome 17p-linked Prostate Cancer Susceptibility  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: 09/434,382  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 224  
LENGTH: 826  
TYPE: PRT  
ORGANISM: Pan troglodytes  
US-09-564-805-224

Query Match 45.5%; Score 5; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CPDES 8  
DB 311 CPDES 315

RESULT 12  
US-09-564-805-226  
Sequence 226, Application US/09564805  
Patent No. 6333403  
GENERAL INFORMATION:  
APPLICANT: Tavligian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Myriad Genetics, Inc.  
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: 09/434,382  
PRIOR FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 226  
LENGTH: 826  
TYPE: PRT  
ORGANISM: Gorilla gorilla

US-09-564-805-226

Query Match 45.5%; Score 5; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CPDES 8  
DB 311 CPDES 315

RESULT 13  
US-09-134-513-2  
Sequence 2, Application US/09134513  
Patent No. 6210964  
GENERAL INFORMATION:  
APPLICANT: Brown, Edward M.  
APPLICANT: Diaz, Ruben  
APPLICANT: Bai, Mei  
APPLICANT: Quinn, Stephen J.  
TITLE OF INVENTION: The Avian Extracellular Calcium Sensing  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Vison & Elkins L.L.P.  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.  
ZIP: 20004-1008  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,513  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanzo, Michael A.  
REGISTRATION NUMBER: 36,912  
REFERENCE/DOCKET NUMBER: BR131/13003  
TELEPHONE: (202)639-6585  
TELEFAX: (202)639-6604  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1059 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
US-09-134-513-2

Query Match 45.5%; Score 5; DB 4; Length 1059;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VDCPD 6  
DB 565 VDCPD 569

RESULT 14  
US-08-633-770A-2  
Sequence 2, Application US/08633770A  
Patent No. 5908760  
GENERAL INFORMATION:  
APPLICANT: Bojsen, Kirsten  
APPLICANT: Yu, Shukun  
APPLICANT: Kragh, Karsten

Thu Apr 17 07:55:19 2003

us-09-897-778-176\_copy\_41\_51.Oligo.ra1

Page 6

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APPLICANT: Christensen, Tove
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU6.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-633-770A-2

Query Match 45.5%; Score 5; DB 2; Length 1070;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESWAL 11
DB 586 ESWAL 590

RESULT 15
US-08-947-823-3
Sequence 3, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isouhli
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-947-823-3

Query Match 45.5%; Score 5; DB 3; Length 1255;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 679 PDESW 683
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GenCore version 5.1.4\_p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	11	100.0	18	10	US-09-897-778-465
3	11	100.0	20	10	US-09-735-705-400
4	11	100.0	20	10	US-09-850-716A-400
5	11	100.0	20	10	US-09-897-778-400
6	11	100.0	20	10	US-09-897-778-457
7	11	100.0	20	10	US-09-735-705-116
8	11	100.0	20	10	US-09-735-705-348
9	11	100.0	20	10	US-09-850-716A-176
10	11	100.0	20	10	US-09-850-716A-348
11	11	100.0	20	10	US-09-897-778-176
12	11	100.0	20	10	US-09-897-778-348
13	11	100.0	20	10	US-09-897-778-446
14	11	100.0	20	10	US-09-897-778-449
15	11	100.0	20	10	US-09-850-716A-427
16	11	100.0	20	10	US-09-897-778-427
17	9	81.8	20	10	US-09-735-705-399
18	9	81.8	20	10	US-09-850-716A-399
19	9	81.8	20	10	US-09-897-778-399

20	7	63.6	577	10	US-09-873-637-2	Sequence 2, Appl1
21	5	45.5	71	10	US-09-864-761-37078	Sequence 37078, A
22	5	45.5	94	10	US-09-789-561-129	Sequence 129, App
23	5	45.5	119	9	US-10-007-270-26	Sequence 26, Appl1
24	5	45.5	150	10	US-09-940-836A-9	Sequence 9, Appl1
25	5	45.5	150	10	US-09-925-300-1535	Sequence 1535, Ap
26	5	45.5	235	10	US-09-803-286A-4	Sequence 4, Appl1
27	5	45.5	294	10	US-10-155-649-2	Sequence 2, Appl1
28	5	45.5	298	10	US-09-815-242-5142	Sequence 5142, Ap
29	5	45.5	303	9	US-09-925-299-851	Sequence 851, App
30	5	45.5	303	10	US-09-925-299-851	Sequence 851, App
31	5	45.5	357	9	US-10-260-877-128	Sequence 128, App
32	5	45.5	357	10	US-09-815-242-10981	Sequence 10981, A
33	5	45.5	412	9	US-10-007-270-19	Sequence 19, Appl1
34	5	45.5	618	10	US-09-815-242-10864	Sequence 10864, A
35	5	45.5	761	9	US-09-147-947-4	Sequence 4, Appl1
36	5	45.5	826	9	US-09-988-626-2	Sequence 2, Appl1
37	5	45.5	826	9	US-09-988-626-224	Sequence 224, App
38	5	45.5	826	9	US-09-988-626-226	Sequence 226, App
39	5	45.5	826	9	US-09-988-687-2	Sequence 2, Appl1
40	5	45.5	826	9	US-09-988-687-224	Sequence 224, App
41	5	45.5	826	9	US-09-988-687-226	Sequence 226, App
42	5	45.5	850	10	US-09-888-615-108	Sequence 108, App
43	5	45.5	1070	9	US-09-423-126-4	Sequence 4, Appl1
44	5	45.5	1070	10	US-09-280-197-6	Sequence 6, Appl1
45	5	45.5	1241	9	US-10-007-270-17	Sequence 17, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-897-778-466  
Sequence 466, Application US/09897778  
Patent No. US2002014713A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnetakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-466  
Query Match 100.0%; Score 11; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4, 2e-07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 FVDCPDSESWAL 11  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong

```

; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 467
; SEQ ID NO: 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 FVDCPDSESWAL 15
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RESULT 3
; Sequence 400, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-400
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```
Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```

RESULT 4
US-09-850-716A-400
; Sequence 400, Application US/09850716A
; Patent No. US20020115139A1
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; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-400
```

```
Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```

RESULT 5
US-09-897-778-400
; Sequence 400, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-400
```

```
Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```

RESULT 6
US-09-897-778-457
; Sequence 457, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
```

```
; APPLICANT: Henderson, Robert A.
; APPLICANT: Beckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-457

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 2 FVDCPDSESMAL 12

RESULT 7
US-09-735-705-176
; Sequence 176, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-176

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 8
US-09-735-705-348
; Sequence 348, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
```

```
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-348

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 9
US-09-850-716A-176
; Sequence 176, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 10
US-09-850-716A-348
; Sequence 348, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
```

```
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-348
```

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Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDSESWAL 11
        |||
Db       41 FVDCPDSESWAL 51
```

```
RESULT 11
US-09-897-778-176
; Sequence 176, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mamerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-176
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```
Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDSESWAL 11
        |||
Db       41 FVDCPDSESWAL 51
```

```
RESULT 12
US-09-897-778-348
; Sequence 348, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mamerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348
```

```
Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 FVDCPDSESWAL 11
        |||
Db       41 FVDCPDSESWAL 51
```

```
RESULT 13
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mamerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446
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Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDSESWAL 11
        |||
Db       41 FVDCPDSESWAL 51
```

```
RESULT 14
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mamerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 449  
LENGTH: 579  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-897-778-449

Query Match  
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;  
Pred. NO. 1,1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDPSWAL 11  
|||||  
Db 41 FVDCPDPSWAL 51

RESULT 15

US-09-850-716A-427  
Sequence 427, Application US/09850716A  
Patent NO. US20020115139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: RETICULAR, MARC W.  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 427  
LENGTH: 586  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-850-716A-427

Query Match  
Best Local Similarity 100.0%; Score 11; DB 10; Length 586;  
Pred. NO. 1,1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDPSWAL 11  
|||||  
Db 48 FVDCPDPSWAL 58

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Job time: 2.26437 secs



GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:34:47 ; Search time 7.45977 Seconds  
(without alignments)  
950.708 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51  
Perfect score: 11  
Sequence: 1 FVDCPESMAL 11

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Gapop 60.0, Gapept 60.0

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27: /cgn2\_6/ptodata/1/paa/US104.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	11	100.0	11	22 US-09-897-778-466	Sequence 466, App
3	11	100.0	11	24 US-10-007-700-466	Sequence 466, App
4	11	100.0	11	25 US-10-117-982-466	Sequence 466, App
5	11	100.0	18	1 PCT-US01-47576-465	Sequence 465, App
6	11	100.0	18	22 US-09-897-778-465	Sequence 465, App

7	11	100.0	18	24	US-10-007-700-465	Sequence 465, App
8	11	100.0	18	25	US-10-117-982-465	Sequence 465, App
9	11	100.0	20	1	PCT-US01-47576-460	Sequence 460, App
10	11	100.0	20	1	PCT-US01-47576-457	Sequence 457, App
11	11	100.0	20	21	US-09-735-705-400	Sequence 400, App
12	11	100.0	20	22	US-09-850-716-400	Sequence 400, App
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16	11	100.0	20	24	US-10-007-700-460	Sequence 460, App
17	11	100.0	20	24	US-10-007-700-457	Sequence 457, App
18	11	100.0	20	25	US-10-117-982-400	Sequence 400, App
19	11	100.0	20	25	US-10-117-982-457	Sequence 457, App
20	11	100.0	43	25	US-10-117-982-482	Sequence 482, App
21	11	100.0	579	1	PCT-US01-47576-176	Sequence 176, App
22	11	100.0	579	1	PCT-US01-47576-348	Sequence 348, App
23	11	100.0	579	1	PCT-US01-47576-446	Sequence 446, App
24	11	100.0	579	1	PCT-US01-47576-449	Sequence 449, App
25	11	100.0	579	18	US-09-466-396A-176	Sequence 176, App
26	11	100.0	579	18	US-09-476-496A-176	Sequence 176, App
27	11	100.0	579	18	US-09-480-884A-176	Sequence 176, App
28	11	100.0	579	19	US-09-510-376A-176	Sequence 176, App
29	11	100.0	579	19	US-09-542-615A-176	Sequence 176, App
30	11	100.0	579	19	US-09-542-615A-348	Sequence 348, App
31	11	100.0	579	20	US-09-606-421A-176	Sequence 176, App
32	11	100.0	579	20	US-09-606-421A-348	Sequence 348, App
33	11	100.0	579	20	US-09-606-421B-176	Sequence 176, App
34	11	100.0	579	20	US-09-606-421B-348	Sequence 348, App
35	11	100.0	579	20	US-09-630-940A-176	Sequence 176, App
36	11	100.0	579	20	US-09-630-940A-348	Sequence 348, App
37	11	100.0	579	20	US-09-630-940B-176	Sequence 176, App
38	11	100.0	579	20	US-09-630-940B-348	Sequence 348, App
39	11	100.0	579	20	US-09-662-786-176	Sequence 176, App
40	11	100.0	579	20	US-09-662-786-348	Sequence 348, App
41	11	100.0	579	20	US-09-685-696-176	Sequence 176, App
42	11	100.0	579	20	US-09-685-696-348	Sequence 348, App
43	11	100.0	579	21	US-09-735-705-176	Sequence 176, App
44	11	100.0	579	21	US-09-735-705-348	Sequence 348, App
45	11	100.0	579	21	US-09-791-537-49019	Sequence 49019, A

## ALIGNMENTS

RESULT 1  
PCT-US01-47576-466  
Sequence 466, Application PC/US0147576

GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tongfong  
APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Beckman, David W.  
APPLICANT: Cai, Feng  
APPLICANT: Foy, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.45503pc  
CURRENT APPLICATION NUMBER: PCT/US01/47576  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US01-47576-466

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11  
DB 1 FVDCPDDESMAL 11

RESULT 2  
US-09-897-778-466  
Sequence 466, Application US/09897778  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnetakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-466

Query Match 100.0%; Score 11; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11  
DB 1 FVDCPDDESMAL 11

RESULT 3  
US-10-007-700-466  
Sequence 466, Application US/10007700  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Vedvick, Gary R.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Peckham, David W.  
APPLICANT: Cai, Feng  
APPLICANT: Foy, Teresa M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C17  
CURRENT APPLICATION NUMBER: US/10/007,700  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-007-700-466

Query Match 100.0%; Score 11; DB 24; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11  
DB 1 FVDCPDDESMAL 11

RESULT 4  
US-10-117-982-466  
Sequence 466, Application US/10117982  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Mericle, Barbara  
APPLICANT: Spies, Gregory A.  
APPLICANT: Pan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C18  
CURRENT APPLICATION NUMBER: US/10/117,982  
CURRENT FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 484  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-117-982-466

Query Match 100.0%; Score 11; DB 25; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11  
DB 1 FVDCPDDESMAL 11

RESULT 5  
PCT-US01-47576-465  
Sequence 465, Application PC/TUS0147576  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tonglong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Fanger, Gary R.



```

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-465

```

```

Query Match          100.0%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 6
US-09-897-778-465
; Sequence 465, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnetakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465

```

```

Query Match          100.0%; Score 11; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 7
US-10-007-700-465
; Sequence 465, Application US/10007700
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.

```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Reller, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Cai, Feng
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-465

```

```

Query Match          100.0%; Score 11; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 8
US-10-117-982-465
; Sequence 465, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-465

```

```

Query Match          100.0%; Score 11; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 9
PCT-US01-47576-400
; Sequence 400, Application PC/TUS0147576

```

```

: GENERAL INFORMATION:
: ORGANISM: Homo sapiens
: PCT-US01-47576-457
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tonglong
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Beckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 400
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US01-47576-400

Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12

RESULT 10
PCT-US01-47576-457
: GENERAL INFORMATION:
: ORGANISM: Homo sapiens
: PCT-US01-47576-457
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tonglong
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Beckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT
```

```

: ORGANISM: Homo sapiens
: PCT-US01-47576-457
Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12

RESULT 11
US-09-735-705-400
: GENERAL INFORMATION:
: ORGANISM: Homo sapiens
: PCT-US01-47576-457
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tonglong
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Beckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 400
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-400

Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12

RESULT 12
US-09-850-716-400
: GENERAL INFORMATION:
: ORGANISM: Homo sapiens
: PCT-US01-47576-457
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tonglong
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Beckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT
```

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 400  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716-400

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
|||||  
DB 2 FVDCPDESVAL 12

RESULT 13  
US-09-850-716A-400  
; Sequence 400, Application US/09850716A  
; GENERAL INFORMATION:  
; APPLICANT: McNeill, Michael D.  
; APPLICANT: Kalos, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 400  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
|||||  
DB 2 FVDCPDESVAL 12

RESULT 14  
US-09-897-778-400  
; Sequence 400, Application US/09897778  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 400  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-400

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FVDCPDESVAL 11  
|||||  
DB 2 FVDCPDESVAL 12

RESULT 15  
US-09-897-778-457  
; Sequence 457, Application US/09897778  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-457

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
|||||  
DB 2 FVDCPDESVAL 12

Search completed: April 16, 2003, 16:45:13  
Job time : 8.45977 secs

2

3

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:35:32 ; Search time 2.27586 Seconds

(without alignments)  
753.673 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 11

Sequence: 1 FVDCPDESMAL 11

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 705215 seqs, 155932251 residues

Word size: 0

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	11	100.0	11	US-10-313-986-466	Sequence 466, App
2	11	100.0	18	US-10-313-986-465	Sequence 465, App
3	11	100.0	20	US-10-313-986-457	Sequence 457, App
4	11	100.0	20	US-10-313-986-457	Sequence 457, App
5	11	100.0	20	US-10-313-986-457	Sequence 457, App
6	11	100.0	43	US-10-313-986-482	Sequence 482, App
7	11	100.0	134	US-09-724-676-92917	Sequence 92917, A
8	11	100.0	134	US-09-724-676-92917	Sequence 92917, A
9	11	100.0	492	US-09-724-676-92916	Sequence 92916, A
10	11	100.0	492	US-09-724-676-92916	Sequence 92916, A
11	11	100.0	358	US-09-724-676-92918	Sequence 92918, A
12	11	100.0	358	US-09-724-676-92918	Sequence 92918, A
13	11	100.0	379	US-10-313-986-176	Sequence 176, App
14	11	100.0	379	US-10-313-986-176	Sequence 176, App
15	11	100.0	379	US-10-313-986-176	Sequence 176, App
16	11	100.0	379	US-10-313-986-176	Sequence 176, App
17	11	100.0	379	US-10-313-986-176	Sequence 176, App
18	11	100.0	379	US-10-313-986-176	Sequence 176, App
19	11	100.0	579	US-10-313-986-448	Sequence 448, App
20	11	100.0	579	US-10-313-986-448	Sequence 448, App
21	11	100.0	589	US-10-313-986-427	Sequence 427, App
22	11	100.0	589	US-10-313-986-427	Sequence 427, App
23	9	81.8	20	US-10-313-986-399	Sequence 399, App
24	9	81.8	20	US-10-313-986-470	Sequence 470, App
25	7	63.6	572	US-09-724-676-48617	Sequence 48617, A
26	7	63.6	572	US-09-724-676-48618	Sequence 48618, A

27	7	63.6	572	US-09-724-676A-48617	Sequence 48617, A
28	7	63.6	572	US-09-724-676A-48618	Sequence 48618, A
29	7	63.6	572	US-09-724-676A-48619	Sequence 48619, A
30	7	63.6	572	US-09-724-676A-48620	Sequence 48620, A
31	7	63.6	598	US-09-724-676A-48621	Sequence 48621, A
32	7	63.6	598	US-09-724-676A-48622	Sequence 48622, A
33	7	63.6	598	US-09-724-676A-48623	Sequence 48623, A
34	7	63.6	602	US-09-724-676A-48624	Sequence 48624, A
35	7	63.6	602	US-09-724-676A-48625	Sequence 48625, A
36	7	63.6	602	US-09-724-676A-48626	Sequence 48626, A
37	7	63.6	602	US-09-724-676A-48627	Sequence 48627, A
38	6	54.5	75	US-09-864-408A-5254	Sequence 5254, A
39	5	45.5	71	US-10-203-138A-14189	Sequence 14189, A
40	5	45.5	73	US-10-366-683-20948	Sequence 20948, A
41	5	45.5	122	PCT-US02-32727-4014	Sequence 4014, A
42	5	45.5	122	US-09-878-825-4014	Sequence 4014, A
43	5	45.5	122	US-10-057-498-4014	Sequence 4014, A
44	5	45.5	144	PCT-US02-32727-19712	Sequence 19712, A
45	5	45.5	144	PCT-US02-32727-19712	Sequence 19712, A

## ALIGNMENTS

```

RESULT 1
: Sequence 466, Application US/10313986
: GENERAL INFORMATION:
: APPLICANT: Foy, Teresa M.
: APPLICANT: McNabb, Andria
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Reed, Steven G.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C19
: CURRENT APPLICATION NUMBER: US/10/313.986
: NUMBER OF SEQ ID NOS: 560
: SOFTWARE: FASTSEQ FOR Windows Version 4.0
: SEQ ID NO 466
: LENGTH: 11
: ORGANISM: Homo sapiens
: US-10-313-986-466

Query Match      100.0%  Score 11: DB 6: Length 11:
Best local similarity 100.0%: Pred. No. 1.4e-07:
Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0,

OY      1 FVDCPDESMAL 11
DB      1 FVDCPDESMAL 11

RESULT 2
: Sequence 465, Application US/10313986
: GENERAL INFORMATION:
: APPLICANT: Foy, Teresa M.
: APPLICANT: McNabb, Andria
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Reed, Steven G.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C19
: CURRENT APPLICATION NUMBER: US/10/313.986
: NUMBER OF SEQ ID NOS: 560
: SOFTWARE: FASTSEQ FOR Windows Version 4.0
: SEQ ID NO 465
: LENGTH: 18

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-465

```

Query Match	100.0%	Score 11;	DB 6;	Length 18;
Best local Similarity	100.0%	Pred. No. 2	2e-07;	
Matches 11; Conservative	0;	Mismatches	0;	Gaps 0;

```

RESULT 3
US-10-313-986-400
Sequence 400, Application US/10313986
CURRENT FILING DATE: 2002-12-04
APPLICANT: Roy, Teresa M.
APPLICANT: McNabb, Andrea
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
INVENTOR: Watanabe, Yoshihiro
TITLE OF INVENTION: CATIONS AND METHODS FOR THE THERAPY
FILE REPRESENTATIVE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SEQUENCE LISTING:
SEQ ID NO. 1: LABELED FOR Windows Version 4.0
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-313-986-400

```

```

Query Match      100.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 4
US-10-313-986-457
US-10-313-986-457 Application US-10313986
GENERAL INFORMATION:
APPLICANT: PCV, Teresa M.
APPLICANT: McNabb, Andita
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tonglong
TITLE OF INVENTION: APPLICATIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US-10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SEQUENCE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 457
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-313-986-457

```

```

Query Match      100.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FVDCPDPSMAL 11
        | | | | | | | |
Db      2 FVDCPDPSMAL 12

```

## RESULT 5

```

1 Sequence 508, Application US/1031986
2 GENERAL INFORMATION:
3 APPLICANT: Foy, Teresa M.
4 APPLICANT: Mcnabb, Andrea
5 APPLICANT: Saito, Shihito
6 APPLICANT: Reed, Steven G
7 APPLICANT: Wang, Tongtong
8 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
9 OF METASTASIS OF LUNG CANCER
10 TITLE OF INVENTION: 102
11 CURRENT FILING DATE: US/10/31986
12 CURRENT FILING DATE: 2002-12-04
13 NUMBER OF SEQ ID NOS: 560
14 SEQ ID NOS: 1-560
15 SEQ ID NOS: 1-560 for Windows Version 4.0
16 LENGTH: 20
17 TYPE: PRT
18 ORGANISM: Homo sapiens
19 US-10-319-986-508

```

Query Match	100.0%	Score 11, DB 6,	length 20,
Best Local Similarity	100.0%	Pred No 2 4e-07,	
Matches 11; Conservative	0,	Mismatches 0,	Indels 0, Gaps 0,

```

RESULT 6
US-10-313-986-482
SEQUENCE 13: Application US/10313986
APPLICANT: NICHOLSON
APPLICANT: POY, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10-313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 42
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-10-313-986-482

```

```

Query Match      100.0%; Score 11, DB 6, length 43,
Best Local Similarity 100.0%; Pred No 4 7e-07,
Matches 11; Conservative 0; Mismatches 0, Indels 0, Gaps 0,

```

RESULT 7  
US-09-724-676-52917  
Sequence 52917, Application US/09724676  
PUBLICATION INFORMATION: LTD  
APPLICANT: LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181, 4 Compuscan  
CURRENT APPLICATION NUMBER US/09/724,676  
CURRENT FILING DATE 2000-11-28

```

; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92917

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 134;
Pred. No. 1.3e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 8
US-09-724-676A-92917
; Sequence 92917, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92917

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 134;
Pred. No. 1.3e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 9
US-09-724-676-92916
; Sequence 92916, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92916

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 492;
Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 10
US-09-724-676A-92916
; Sequence 92916, Application US/09724676A
; GENERAL INFORMATION:

```

```

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92916

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 492;
Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 11
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 558;
Pred. No. 4.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 12
US-09-724-676A-92918
; Sequence 92918, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92918

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 558;
Pred. No. 4.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

```

```
RESULT 13
US-10-313-986-176
; Sequence 176, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; CURRENT APPLICATION NUMBER: US/10/313,986
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

RESULT 14
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; CURRENT APPLICATION NUMBER: US/10/313,986
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

RESULT 15
US-10-313-986-446
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

```
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-446

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51
```

Search completed: April 16, 2003, 16:47:26  
Job time : 3.27586 secs



GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:31:34 ; Search time 0.704434 Seconds  
(without alignments)  
1501.176 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 11

Sequence: 1 FVDCPDESMAL 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR.73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	54.5	75	2	G97116
2	6	54.5	234	2	A12709
3	6	54.5	234	2	B97492
4	6	54.5	310	2	T44857
5	6	54.5	313	2	G84335
6	6	54.5	337	2	T30601
7	6	54.5	460	2	G84246
8	5	45.5	88	2	D87272
9	5	45.5	101	2	A82121
10	5	45.5	107	2	AG2581
11	5	45.5	112	2	E97363
12	5	45.5	118	2	T31213
13	5	45.5	133	2	S74640
14	5	45.5	136	2	T35632
15	5	45.5	140	2	B81146
16	5	45.5	160	2	C81877
17	5	45.5	164	2	T19795
18	5	45.5	182	2	B72689
19	5	45.5	190	2	E95420
20	5	45.5	196	2	T19794
21	5	45.5	198	2	E70357
22	5	45.5	214	2	AC2726
23	5	45.5	217	2	AB2491
24	5	45.5	229	2	G97507
25	5	45.5	230	2	JC5418
26	5	45.5	246	2	AD3574
27	5	45.5	261	1	S58496
28	5	45.5	269	1	I55969
29	5	45.5	269	2	G96925

30	5	45.5	270	2	D72334	sugar kinase, pfkB
31	5	45.5	293	2	B64339	spermidine synthas
32	5	45.5	294	1	Q4ADC2	early E4 34k prote
33	5	45.5	294	2	A05071	pol polyprotein -
34	5	45.5	298	2	H83163	probable transcrip
35	5	45.5	307	2	T24832	hypothetical prote
36	5	45.5	324	2	B86819	oxidoreductase yj
37	5	45.5	328	1	S52352	glucose kinase - S
38	5	45.5	328	2	B89935	glucokinase (Impor
39	5	45.5	347	2	F70851	probable parb prot
40	5	45.5	357	1	G64053	chorismate synthas
41	5	45.5	359	2	S27788	neutrophil oxidase
42	5	45.5	371	2	B69451	conserved hypothet
43	5	45.5	379	2	T41947	hypothetical prote
44	5	45.5	383	2	F90415	conserved hypothet
45	5	45.5	409	2	G90491	conserved hypothet

## ALIGNMENTS

## RESULT 1

G97116 probable nucleic acid binding protein, containing KH domain [Imported] - Clostridium

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 17-May-2002

C:Accession: G97116

R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: G97116

A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-75 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK79722.1; PID:g15024725; GSPDB:GN00168

A:Genetic sources: Clostridium acetobutylicum ATCC824

A:Gene: CAC1756

C:Superfamily: Bacillus conserved hypothetical protein y1qc

Query Match 54.5%; Score 6; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPDE 7  
Db 13 VDCPDE 18

## RESULT 2

A12709 branched-chain amino acid permease Atu1082 [Imported] - Agrobacterium tumefaciens (st

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Mar-2002

C:Accession: A12709

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCl  
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: A12709

A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-234 <KUR>  
A:Cross-references: GB:AE008688; PIDN:AAL42095.1; PID:g17739477; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:  
A:Gene: Atu1082

A:Map position: circular chromosome  
C:Superfamily: hypothetical protein b2682

Query Match 54.5%; Score 6; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DESMAL 11  
DB 113 DESMAL 118

#### RESULT 3

B97492 azIC family protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 01-Mar-2002

C:Accession: B97492

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Onorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Mairfeld, B.; Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A:Reference number: A97359; PMID:11743194

A:Accession: B97492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE007869; PIDN:AK6891.1; PID:915156113; GSPDB:GN00169

A:Gene: AGR\_C 2001

A:Map position: circular chromosome

C:Superfamily: hypothetical protein b2682

Query Match 54.5%; Score 6; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DESMAL 11  
DB 113 DESMAL 118

#### RESULT 4

T44857 probable hydroxylase d [imported] - Amycolatopsis orientalis (fragment)  
C:Species: Amycolatopsis orientalis  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 16-Feb-2001

C:Accession: T44857

R:Solenberg, P.J.; Matsushima, P.; Stack, D.R.; Wilkie, S.C.; Thompson, R.C.; Balcz, R.; submitted to the EMBL Data Library, January 1997

A:Description: Production of hybrid glycopeptide antibiotics in vitro and in Streptomyces

A:Reference number: 222861

A:Accession: T44857

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-310 <SOL>

A:Cross-references: EMBL:U84350; PIDN:AAA9296.1

A:Experimental source: strain C129.4

C:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology

F:146-282/Domain: cytochrome P450 homology <P45>

Query Match 54.5%; Score 6; DB 2; Length 310;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPD 6  
DB 299 FVDCPD 304

#### RESULT 5

G84335 hypothetical protein Vng1845c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: G84335

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.;

A:Title: Genome sequence of Halobacterium species NRC-1

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: G84335

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-313 <SNO>

A:Cross-references: GB:AE004437; NID:910581291; PIDN:ANG20051.1; GSPDB:GN00138

C:Gene: VNG1845C

Query Match 54.5%; Score 6; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DESMAL 11  
DB 186 DESMAL 191

#### RESULT 6

T30601 cytochrome P450 hydroxylase homolog PCZA361.27 - Amycolatopsis orientalis (fragment)  
N:Alternate names: PCZA361.27

C:Species: Amycolatopsis orientalis

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 16-Feb-2001

C:Accession: T30601

R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Leonard

Chem. Biol. 3, 155-162, 1998

A:Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin

A:Reference number: 218804

A:Accession: T30601

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-337 <VAN>

A:Cross-references: EMBL:A1223998

C:Superfamily: Bacillus cytochrome P450 homology <P45>

F:173-309/Domain: cytochrome P450 homology <P45>

Query Match 54.5%; Score 6; DB 2; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPD 6  
DB 326 FVDCPD 331

#### RESULT 7

G84246 phosphomannomutase [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C:Accession: G84246

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.;

A:Title: Genome sequence of Halobacterium species NRC-1

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: G84246

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-460 <STO>

A:Cross-references: GB:AE004437; NID:910580465; PIDN:ANG19339.1; GSPDB:GN00138

C:Genetics:  
A:Gene: pmu2  
C:Superfamily: phosphonomonotase

Query Match  
Best Local Similarity 54.5%; Score 6; DB 2; Length 460;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 7  
DB 379 VDCPD 384

RESULT 8  
DB27272

hypothetical protein CC0189 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: DB27272

R:NIEMAN, W.C.; FELDBLYUM, T.V.; PAULSEN, I.T.; NELSON, K.E.; EISEN, J.; HEIDELBERG, J.B.; LAUB, M.T.; DESOY, R.T.; DODSON, R.J.; DURKIN, A.S.; GWINN, M.L.; HAFT, D.H.; KOLTON, J.; ERMOLAIEVA, M.; WHITE, O.; SALZBERG, S.L.; SHAPIRO, L.; VENTER, J.C.; FRASER, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: AB7249; MUID:21173698; PMID:11259647

A:Accession: DB27272

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-88 <STO>

A:Cross-references: GB:AE005673; MUD:913421310; PIDN:AAK22176.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0189

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCP 5  
DB 55 FVDCP 59

RESULT 9  
AH2121

hypothetical protein alr2527 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AH2121

R:KANeko, T.; NAKAMURA, Y.; Wolk, C.P.; KURTZ, T.; SASAMOTO, S.; MATANABE, A.; IRIUCHI, NAKAZAKI, N.; SHIMPO, S.; SUGIMOTO, M.; TAKAZAWA, M.; YAMADA, M.; TABATA, S. DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2121

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA874226.1; PID:917131619; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr2527

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 101;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6  
DB 44 VDCPD 48

RESULT 10

AG2581

phosphoribosyl-ATP pyrophosphohydrolase hlsE [imported] - *Agrobacterium tumefaciens* (s)

C:Species: *Agrobacterium tumefaciens*

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002

C:Accession: AG2581

R:WOOD, D.W.; SETUBAL, J.C.; KAUL, R.; MONKS, D.; CHEN, L.; WOOD, G.E.; CHEN, Y.; WOODERGER, G.; GILLET, W.; GRANT, C.; GUENTHER, D.; KUTYAVIN, T.; LEVY, R.; LI, M.; MCCLELLAN, P.; ROMERO, P.; ZHANG, S. Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamster, E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG2581

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAU41069.1; PID:917738357; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: hlsE

A:Map position: circular chromosome

C:Superfamily: phosphoribosyl-ATP pyrophosphatase hlsE

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 107;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PDESW 9  
DB 21 PDESW 25

RESULT 11  
E97363

phosphoribosyl-ATP pyrophosphatase (PRA-PH) [imported] - *Agrobacterium tumefaciens* (s)

C:Species: *Agrobacterium tumefaciens*

C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002

C:Accession: E97363

R:GOODNER, B.; HINKLE, G.; GATTUNG, S.; MILLER, N.; BLANCHARD, M.; QUROLLO, B.; GOLDMANN, A.; LIU, F.; WOLLAM, C.; ALLINGER, M.; DOUGHTY, D.; SCOTT, C.; LAPPAS, C.; MARKELT, Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*

A:Reference number: A97359; PMID:11743194

A:Accession: E97363

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK85862.1; PID:915154901; GSPDB:GN00169

C:Genetics:

A:Gene: AGR\_C\_60

A:Map position: circular chromosome

C:Superfamily: phosphoribosyl-ATP pyrophosphatase hlsE

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 112;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PDESW 9  
DB 26 PDESW 30

RESULT 12  
T31213

hypothetical protein 724 - *Sphingomonas aromaticivorans* plasmid pML1

C:Species: *Sphingomonas aromaticivorans*

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T31213

R:ROMINE, M.F.; STILLWELL, L.C.; WONG, K.K.; THURSTON, S.J.; SISK, E.C.; SENSEN, C.W. submitted to the EMBL Data Library, July 1998

A:Description: Complete sequence of a 184 kb catabolic plasmid from *Sphingomonas* arom

A:Reference number: Z20992

A:Accession: T31213  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-118 <ROM>  
A:Cross-references: EMBL:AF079317; NID:93378261; PID:93378354; PIDN:AAD03937.1  
C:Genetics:  
A:Gene: plasmid pNL1  
A:Note: orf724  
C:Superfamily: Sphingomonas aromaticivorans plasmid pNL1 hypothetical protein 724

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 118;  
100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 DCPDE 7  
|||||  
Db 87 DCPDE 91

RESULT 13  
S74640  
hypothetical protein slr1780 - Synechocystis sp. (strain PCC 6803)  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S74640  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
S.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S74640  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-133 <KAN>  
A:Cross-references: EMBL:D90900; GB:AB001339; NID:91651768; PIDN:BA016792.1; PID:9165186  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: hypothetical protein slr1780

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 133;  
100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ESNAL 11  
|||||  
Db 2 ESNAL 6

RESULT 14  
T35632  
probable transposase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 18-Aug-2000  
C:Accession: T35632  
R:Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, June 1999  
A:Reference number: 221584  
A:Accession: T35632  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-136 <SEE>  
A:Cross-references: EMBL:AL079356; PIDN:CAB45627.1; GSPDB:GN00070; SCOEDB:SC6G9.36C  
C:Genetics:  
A:Gene: SCOEDB:SC6G9.36C  
C:Superfamily: Streptomyces coelicolor probable transposase SC6G9.36C

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 136;  
100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DESMA 10  
|||||  
Db 15 DESMA 19

RESULT 15  
B81146  
ZnL-related protein NMB0892 [imported] - Neisseria meningitidis (strain MC58 serogro  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: B81146  
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.  
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Pizzi, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: B81146  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140 <RET>  
A:Cross-references: GB:AE002441; GB:AE002098; NID:97226123; PIDN:AAFA1301.1; PID:9722  
C:Genetics:  
A:Gene: NMB0892

Query Match  
Best Local Similarity 45.5%; Score 5; DB 2; Length 140;  
100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DESMA 10  
|||||  
Db 94 DESMA 98

Search completed: April 16, 2003, 16:37:41  
Job time : 2.70443 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:23:10 : Search time 0.559934 Seconds  
(without alignments)  
814.809 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 11  
Sequence: 1 FVDCPDESMAL 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	54.5	75	YH56_CLOAB	Q07196 clostridium
2	5	45.5	107	HIS2_AGR5	Q08J91 agrobacteri
3	5	45.5	133	Y54L_SYN3	P72717 synechocyst
4	5	45.5	174	ARR6_XENLA	P51645 xenopus lae
5	5	45.5	230	SOML_CARAU	P79697 carassius a
6	5	45.5	261	AXTA_ARATH	Q38828 arabidopsis
7	5	45.5	268	IL1B_RAT	Q63264 rattus norv
8	5	45.5	269	IL1B_MOUSE	P10749 mus musculi
9	5	45.5	293	SPEE_METJA	Q57761 methanococc
10	5	45.5	294	E434_ADE02	P03339 human adeno
11	5	45.5	294	POL_SMSAV	P03359 simlan sarc
12	5	45.5	328	GLK_STRXY	Q56198 staphylococ
13	5	45.5	357	AROC_HAEIN	P43875 haemophilus
14	5	45.5	379	DUT_HSV7J	P52241 human hepe
15	5	45.5	431	YAZ1_SCHPO	Q10223 schizosacch
16	5	45.5	439	IF2G_ENCCU	Q96719 encephalito
17	5	45.5	446	IF2G_SCHPO	Q09130 schizosacch
18	5	45.5	471	IF2G_HUMAN	P41091 homo sapien
19	5	45.5	471	IF2G_MOUSE	Q920n1 mus musculi
20	5	45.5	471	IF2H_MOUSE	Q920n2 mus musculi
21	5	45.5	471	MANC_KLEPN	Q48462 klebsiella
22	5	45.5	471	MANC_SALMO	Q01410 salmonella
23	5	45.5	471	RFM9_ECOLI	P37753 escherichia
24	5	45.5	473	FLIT_AGR5	Q34171 agrobacteri
25	5	45.5	473	IF2G_DROME	Q24208 drosophila
26	5	45.5	493	YKAY_CAEEL	P34258 caenorhabdi
27	5	45.5	527	IF2G_YEAST	P32481 saccharomyc
28	5	45.5	545	SYK_STRCO	Q9x895 streptomyce
29	5	45.5	677	SP87_DICDI	P54643 dictyosteli
30	5	45.5	761	NEFR_MOUSE	Q08762 mus musculi
31	5	45.5	1165	POL_GALV	P21414 gibbon ape
32	5	45.5	1173	DPOL_RCMVM	Q85428 rat cytomeg
33	5	45.5	1377	RP0C_BORBU	Q51349 borrelia bu

34	5	45.5	1419	1	LYS2_SCHPO	P40976 schizosacch
35	5	45.5	1471	1	MY54_YEAST	P32492 saccharomyc
36	5	45.5	1628	1	MY58_CLOPE	P26831 clostridium
37	5	45.5	2359	1	CCAH_RAT	Q9e650 rattus norv
38	5	45.5	2365	1	CCAH_MOUSE	Q86427 mus musculi
39	4	36.4	29	1	SCX2_LE10H	P80670 le1urus qui
40	4	36.4	29	1	SCX3_LE10H	P80671 le1urus qui
41	4	36.4	30	1	CRG2_SCOMA	P19865 scoliodon w
42	4	36.4	36	1	PSBY_ODOS1	P49543 odontella s
43	4	36.4	58	1	FE12_HSV2	P14345 herpes simp
44	4	36.4	65	1	TSYL_DENPO	P25518 dendroaspis
45	4	36.4	65	1	TXM2_NAJKA	P82463 naja naja k

## ALIGNMENTS

RESULT 1	YH56_CLOAB	STANDARD	PRT	75 AA.
AC	Q07196:			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hypothetical protein CAC1756.			
GN	CAC1756.			
OS	Clostridium acetobutylicum.			
OC	Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OX	Clostridium.			
NC	NCBI_TaxID=1488;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;			
RX	MEDLINE=21359325; PubMed=11466286;			
RA	Noelling J., Breton G., Melchenko M.V., Makarova K.S., Zeng Q.,			
RA	Gidsov R., Lee H.W., Dubois J., Qiu D., Hitt J., Wolf Y.I.,			
RA	Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,			
RA	Bennett G.N., Koonin E.V., Smith D.R.;			
RT	"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";			
RT	J. Bacteriol. 183:4823-4838(2001).			
RL	J. Bacteriol. 183:4823-4838(2001).			
CC	- SIMILARITY: BELONGS TO THE UPF0109 FAMILY.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
DR	EMBL: AE007684; AAK79722.1;			
DR	PROSITE: PS50084; KH.TYPE.1; FALSE NEG.			
KW	Hypothetical protein; RNA-binding; Complete proteome.			
FT	DOMAIN			
FT	29			
FT	75			
FT	KH.			
FT	SEQUENCE 75 AA: 8170 MW; A68E2113FAFE2DE CRC64;			
Query Match		54.5%;	Score 6;	DB 1;
Best Local Similarity		100.0%;	Pred. No. 0.53;	
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
OY	2 VDCPDE 7			
DB	13 VDCPDE 18			
RESULT 2				
HIS2_AGR5	STANDARD:	PRT:	107 AA.	
ID	HIS2_AGR5			
AC	Q80J91:			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			

DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH).  
OS HISE OR ATU00138 OR AGR\_C\_160.  
OC Agrobacterium tumefaciens (Strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizodium.  
OX NCBI\_TaxId=176239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193;  
RA Wood D.W., Seubert J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okuda D.V., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D., Str.,  
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
RA Raybavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
RA Raymond C., Rouse G., Saenphummacol C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao L., Bidde P., Jung M., Krespan V., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendick C., Zhao Z.-Y., Dolan M.,  
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Neester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
RT C58." ;  
RL Science 294:2317-2323(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608551; PubMed=11743194;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Qurollo B., Goldman B.S., Cao Y., Askrenzi M., Halling C., Mullin L.,  
RA Houmel K., Gordon J., Vaughn M., Tatchou O., Epp A., Liu F.,  
RA Hollam C., Allinger M., Doughy D., Scott C., Iappas C., Merkely B.,  
RA Flanagan C., Crowell C., Gurson J., Lomo C., Seat C., Strud G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
RT Agrobacterium tumefaciens C58." ;  
RL Science 294:2323-2328(2001).  
CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-  
CC phosphoribosyl)-AMP + diphosphate.  
CC -1- PATHWAY: Histidine biosynthesis; second step.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
CC -1- SIMILARITY: BELONGS TO THE PRA-PH FAMILY.  
-----  
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-----  
DR EMBL: AE008978; AAL41069.1; .  
DR EMBL: AE007946; AKR85862.1; ALT\_INIT.  
KW Histidine biosynthesis; Hydrolase; Complete proteome.  
SQ SEQUENCE 107 AA; 11411 MW; 95003B10A6FC6A89 CRC64;  
  
Query Match 45.5%; Score 5; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0;  
  
QY 5 PDESM 9 0; Indels 0; Caps 0;  
Db 21 PDESM 25  
  
RESULT 3  
Y54L\_SYNV3  
ID Y54L\_SYNV3 STANDARD: PRT; 133 AA.  
AC P72777;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Vcf54-like protein.  
GN SUR1780.  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chlorococcales; Synechocystis.

OX	NCBI_TaxID=1148;
(1)	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97061201; PubMed=8905231;
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA	Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA	Hosouchi T., Matsuo A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA	Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA	Takata S.;
RT	Sequence analysis of the genome of the unicellular cyanobacterium
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT	entire genome and assignment of potential protein-coding regions.";
RL	DNA Res. 3:109-136(1996).
-1-	SIMILARITY: BELONGS TO THE YCP54 FAMILY.
CC	
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )
CC	or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> .
DR	EMBL: D90900; BAA16792.1;
KM	Hypothetical protein: Complete proteome.
SO	SEQUENCE 133 AA; 15456 MW; 8655B530E678838 CRC64;
Gy	Query Match 45.5%; Score 5; DB: 1; Length 133;
Db	Best Local Similarity 100.0%; Match No. 14;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	7 ENSAL 11
	2 ENSAL 6
RESULT 4	
ARF6_XENLA	STANDARD: PRT; 174 AA.
ID ARF6_XENLA	
AC F51645;	
DT 01-OCT-1996 (rel. 34, Created)	
DT 01-OCT-1996 (rel. 34, Last sequence update)	
DT 13-JUL-1999 (rel. 38, Last annotation update)	
DE ADP-fibrosylation factor 6.	
GN ARF6.	
OS Xenopus laevis (African clawed frog).	
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;	
OC Xenopodinae; Xenopus.	
OX NCBI_TaxID=83355;	
[1]	
RP	SEQUENCE FROM N.A.
RA	Boman A.L.;
RL	Submitted (JUL-1995) to the EMBL/GeneBank/DDBI databases.
CC	-1- FUNCTION: GTP-BINDING PROTEIN THAT FUNCTIONS AS AN ALLOSTERIC
CC	ACTIVATOR OF THE CHOLERA TOXIN CATALYTIC SUBUNIT AN ADP-
CC	RIBOSYLTRANSFERASE. INVOLVED IN PROTEIN TRAFFICKING. MAY MODULATE
CC	VEHICLE BUDDING AND UNCOATING WITHIN THE GOLGI APPARATUS (BY
CC	SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE ARF FAMILY OF GTP-BINDING PROTEINS.
CC	
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CC	or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> .
DR	EMBL: U31469; AAA74952.1;
DR	HSSP: P32889; IRRE.
DR	InterPro: IPR000251; ARF_family.
DR	InterPro: IPR003225; Small_GTP.

DR InterPro: IPR003575; Small\_GTPase.  
 DR Pfam: PF00025; arf. 1.  
 DR SMART: SM00177; ARF. 1.  
 DR SMART: SM00010; small\_GTPase. 1.  
 DR TRIPFAMS: TRIPR00231; small\_GTP. 1.  
 DR PROSITE: PS01019; ARF. 1.  
 DR GTP-binding: Multigene family; Myristate: Protein transport;  
 KM Gold stack.  
 FT INIT\_MER 0 0 BY SIMILARITY.  
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 FT NP\_BIND 19 26 GTP (BY SIMILARITY).  
 FT NP\_BIND 62 66 GTP (BY SIMILARITY).  
 FT NP\_BIND 121 124 GTP (BY SIMILARITY).  
 SQ SEQUENCE 174 AA; 20056 MW; A6DA35CDADDF1A21 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 5; DB 1; Length 174;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6  
 11111  
 DB 87 VDCPD 91

RESULT 5  
 SOML\_CARAU STANDARD; PRT; 230 AA.  
 ID SOML\_CARAU STANDARD; PRT; 230 AA.  
 AC P79697;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Somatolactin precursor (St).  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 NC NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97242175; PubMed-9125164;  
 RA Cheng K.W., Chan Y.H., Chen Y.D., Yu K.L., Chan K.M.;  
 RT "Sequence of a cDNA clone encoding a novel somatolactin in goldfish,  
 Carassius auratus".  
 RL Biochem. Biophys. Res. Commun. 232:282-287(1997).  
 CC CC  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE SOMATROPIN/PROLACTIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U72940; AAC60098.1; -.  
 DR HSSP: F01246; IBST.  
 DR InterPro: IPR001230; Ptenyl\_site.  
 DR InterPro: IPR001400; Somatolactin.  
 DR Pfam: PF00103; hormone. 1.  
 DR PROSITE: PS00266; SOMATOTROPIN\_1; FALSE\_NEG.  
 DR PROSITE: PS00338; SOMATOTROPIN\_2; 1.  
 DR Hormone: Glycoprotein; signal.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 1 23 SOMATOLACTIN.  
 FT DISULFID 28 38 BY SIMILARITY.  
 FT DISULFID 87 202 BY SIMILARITY.  
 FT DISULFID 219 227 BY SIMILARITY.  
 FT CARBOHYD 226 226 BY SIMILARITY.  
 SQ SEQUENCE 230 AA; 25735 MW; CBC5DB3476116DC CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 5; DB 1; Length 230;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6  
 11111  
 DB 26 VDCPD 30

RESULT 6  
 AXIA\_ARATH STANDARD; PRT; 261 AA.  
 ID AXIA\_ARATH STANDARD; PRT; 261 AA.  
 AC Q38828;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Auxin-responsive protein IAA10 (Indoleacetic acid-induced protein 10).  
 GN IAA10 OR ATIG04100 OR F20D22.13.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE-95387393; PubMed-7658471;  
 RA Abel S., Nguyen M.D., Theologis A.;  
 RT "The PS-IAA4/5-like family of early auxin-inducible mRNAs in  
 Arabidopsis thaliana".  
 RL J. Mol. Biol. 251:533-549(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE-21016719; PubMed-11130712;  
 RA Theologis A., Ecker J.R., Palm C.D., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kuan A., Lam B.,  
 RA Lander-Hopfer S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Juros J.S., Maiti R., Marzilli A.,  
 RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Taiton L.J., Tambunga G., Tortum M.J., Town C.D.,  
 RA Ullrichbeck T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana".  
 RL Nature 408:816-820(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Ban J., Etgu P., Lee J.M.,  
 RA Tortum M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,  
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,  
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;  
 RT "Full length cDNA of gene F20D22.13 (GI:3142299)".  
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 CC CC  
 CC -1- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR  
 CC MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR CELL  
 CC GROWTH (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- INDUCTION: BY AUXIN.  
 CC -1- SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.  
 CC -----  
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CC -----  
DR EMBL: U18412; AAC49051.1; -  
DR EMBL: AC002411; AAC16750.1; -  
DR EMBL: AF333396; AAG48760.1; -  
DR InterPro: IPR003111; AUX\_1AA.  
DR Pfam: PF02309; AUX\_1AA; 1.  
KW Multigene family; Nuclear protein; Translation regulation.  
FT DOMAIN 60  
FT SEQUENCE 261 AA; 27878 MW; DE9919434815A14 CRC64;  
SO  
Query Match 45.5%; Score 5; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 CPDES 8  
DB 35 CPDES 39  
RESULT 7  
IL1B\_RAT  
ID IL1B\_RAT STANDARD; PRT; 268 AA.  
AC 063264;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN IL1B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Macrophage;  
RA Feiser W., Frelmark B.D.;  
RL Submitted (Aug-1992) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -1- MISCELLANEOUS: THESE PROTEINS SERVE AS YET UNDEFINED FUNCTION.  
CC PRECURSOR SEQUENCE BY A MECHANISM THAT IL-1 IS RELEASED BY DAMAGED CELLS  
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY  
CC -----  
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CC -----  
DR EMBL: M98820; AAA41426.1; -  
DR HSSP: P10749; 2M1B.  
DR InterPro: IPR002348; IL1\_HRGF.  
DR InterPro: IPR000502; IL1\_propop.  
DR InterPro: IPR000975; Interleukin\_1.  
DR Pfam: PF00340; IL1; 1.  
DR Pfam: PF02394; IL1\_propop; 1.  
DR PRINTS: PR00262; IL1HRGF.  
DR PRODOM: PD002536; Interleukin\_1; 1.  
DR SMART: SM00125; IL1; 1.  
DR POSITE: PS00253; INTERLEUKIN\_1; 1.

KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
FT PROPEP 116  
FT CHAIN 117  
SQ SEQUENCE 268 AA; 30644 MW; 109C19B8F9C242D CRC64;  
SO  
Query Match 45.5%; Score 5; DB 1; Length 268;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 CPDES 8  
DB 42 CPDES 46  
RESULT 8  
IL1B\_MOUSE  
ID IL1B\_MOUSE STANDARD; PRT; 269 AA.  
AC P10749;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN IL1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=87058957; PubMed=3491144;  
RA Gray P.W., Glaister D., Chen E., Goeddel D.V., Pennica D.;  
RT "Two interleukin 1 genes in the mouse: cloning and expression of the  
RT cDNA for murine interleukin 1 beta."  
RL J. Immunol. 137:3644-3648(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87117546; PubMed=3492706;  
RX Telford J.L., Macchia G., Massone A., Carinci V., Palla E., Meili M.;  
RT "The murine interleukin 1 beta gene: structure and evolution."  
RL Nucleic Acids Res. 14:9955-9963(1986).  
RN [3]  
RP SEQUENCE OF 118-139.  
RA MEDLINE=88229074; PubMed=2967326;  
RA Huang J.J., Newton R.C., Rutledge S.J., Horuk R., Mathew J.B.,  
RA Coughlin M., Lin Y.;  
RT "Characterization of murine IL-1 beta. Isolation, expression, and  
RT purification."  
RL J. Immunol. 140:3838-3843(1988).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=92222792; PubMed=1807351;  
RX van Oostum J., Priesle J.P., Grutter M.G., Schmitz A.;  
RA "The structure of murine interleukin 1 beta at 2.8-A resolution."  
RL J. Biol. Chem. 268:19519-19528(1993).  
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -1- MISCELLANEOUS: THESE PROTEINS SERVE AS YET UNDEFINED FUNCTION.  
CC PRECURSOR SEQUENCE BY A MECHANISM THAT IL-1 IS RELEASED BY DAMAGED CELLS  
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC -----  
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RP SEQUENCE FROM N.A. / DSM 2661 / ATCC 43067;
RX STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868887;
RA Raution G.G., White O., Olsen G.J., Zhou L., Fleischman R.D.,
RA Bolt C.J., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Overbeek A.R., Dougherty F.B., Tomb J.-F., Adams M.D., Reisch C.I.,
RA Scott J.L., Geoghegan N.S.M., Waidman J.F., Fuhrman J.L., Nguyen D.,
RA Utechback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.P., Roberts C.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii."
RL Science 273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY: S'-adenosylmethioninamine + putrescine = 5'-
CC methylthioadenosine + spermidine.
CC -1- PATHWAY: FIFTH (LAST) STEP IN THE BIOSYNTHESIS OF SPERMIDINE FROM
CC ARGININE AND METHIONINE.
CC -1- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
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CC
DR EMBL: U67486; AAB98300.1; -.
DR TIGR: MJD0313; -.
DR InterPro: IPR000051; SAM_bind.
DR InterPro: IPR001045; Spmrline_synthase.
DR Pfam: PF01564; Spermrline_synth; 1.
DR TIGRFAMs: TIGR00417; speed; 1.
DR PROSITE: PS01330; SPERMIDINE_SYNTHASE; 1.
KW Spermidine biosynthesis; Transferrase; Complete proteome.
FT DOMAIN 85 126
FT BINDING TO DECARBOXYLATED SAM (POTENTIAL).
SO SEQUENCE 293 AA; 33899 MW; 88E4A8C919E5452A CRC64;

Query Match 45.5%; Score 5; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6
| | | |
DB 162 VDCPD 166

RESULT 10
E434_ADE02 STANDARD; PRT; 294 AA.
ID E434_ADE02
AC P03239;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE Early E4 34 kDa protein.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059444; PubMed=6985482;
RA Herisse J., Rispolet M., Dupont de Dinechin S., Galibert F.;
RT "Nucleotide sequence of adenovirus 2 DNA fragment encoding for the
RT carboxylate region of the fiber protein and the entire E4 region."
RL Nucleic Acids Res. 9:4023-4042(1981).
CC -1- MISCELLANEOUS: FOUND IN ASSOCIATION WITH E1B 55 KDA PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN
CC FAMILY.
CC
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 CC -----  
 DR EMBL: J01917; NOT\_ANNOTATED\_CDS.  
 DR PIR: A03805; Q4ADC2.  
 KW Early protein.  
 SQ SEQUENCE 294 AA; 34116 MW; F60C83A38240BE0C CRC64;

Query Match 45.5%; Score 5; DB 1; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ESWAL 11  
 Db 118 ESWAL 122

RESULT 11  
 ID POL\_SMSAV STANDARD; PRT; 294 AA.

AC P03359;  
 DT 21-JUL-1986 (rel. 01, Created)  
 DT 21-JUL-1986 (rel. 01, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE POL. polyprotein (Contains: Reverse transcriptase (EC 2.7.7.49))  
 DE (fragment).  
 DE  
 GN POL.  
 OS Simian sarcoma virus.  
 OS Viruses; Retroviridae; Gammaretrovirus.

CC EMBL: X84332; CAAS9069.1;  
 CC InterPro: IPR000600; ROK\_family.  
 CC InterPro: IPR004654; ROK\_glaA\_fam.  
 CC Pfam: PF00480; ROK; 1.  
 CC TIGRFAMs: TIGR00744; ROK\_glaA\_fam; 1.  
 CC PROSITE: PS01125; ROK; 1.  
 CC Transferrase; Kinase; Glycolysis; ATP-binding.  
 KW SEQUENCE 328 AA; 35032 MW; 9BF622D66A1B5DF CRC64;

Query Match 45.5%; Score 5; DB 1; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCP 5  
 Db 105 FVDCP 109

RESULT 13  
 ID AROC\_HAEIN STANDARD; PRT; 357 AA.

AC 056198;  
 DT 15-JUL-1998 (rel. 36, Created)  
 DT 15-JUL-1998 (rel. 36, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Glucokinase (EC 2.7.1.2) (Glucose kinase).  
 DE GLKA.  
 OS Staphylococcus xylosous.  
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 CC NCBI\_TaxID=1288;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 20267 / Isolate CZA;  
 RX MEDLINE=96042090; PubMed=7592379;  
 RA Wagner E., Marcandier S., Egster O., Deutscher J., Goetz F.,  
 RA Brueckner R.;  
 RT "Glucose kinase-dependent catabolite repression in Staphylococcus  
 RT xylosous".  
 RT J. Bacteriol. 177:6144-6152(1995).  
 CC -1- CATALYTIC ACTIVITY: ATP + D-glucose -> ADP + D-glucose 6-phosphate.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ROK (NAGC/XLR) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X84332; CAAS9069.1;  
 DR InterPro: IPR000600; ROK\_family.  
 DR InterPro: IPR004654; ROK\_glaA\_fam.  
 DR Pfam: PF00480; ROK; 1.  
 DR TIGRFAMs: TIGR00744; ROK\_glaA\_fam; 1.  
 DR PROSITE: PS01125; ROK; 1.  
 DR Transferrase; Kinase; Glycolysis; ATP-binding.  
 KW SEQUENCE 328 AA; 35032 MW; 9BF622D66A1B5DF CRC64;

Query Match 45.5%; Score 5; DB 1; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PDESW 9  
 Db 268 PDESW 272

RESULT 12  
 ID GLK\_STAXY STANDARD; PRT; 328 AA.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J01917; NOT\_ANNOTATED\_CDS.  
 DR PIR: A03805; Q4ADC2.  
 KW Early protein.  
 SQ SEQUENCE 294 AA; 34116 MW; F60C83A38240BE0C CRC64;

```

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.:
RT "Whole-genome random sequencing and assembly of Hemophilus influenzae
RT Rd.".
RL Science 269:496-512(1995).
CC -1- CATALYTIC ACTIVITY: 5-O-(1-carboxyvinyl)-3-phosphoshikimate =
CC chorismate + phosphate.
CC -1- COFACTOR: REDUCED FLAVIN (BY SIMILARITY).
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC seventh step.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
CC -----
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CC -----
CC
CC EMBL: U3704; AAC21865.1; -
CC TIGR: H10196; -
CC InterPro: IPR000453; Chorismate_synth.
CC Pfam: PF01264; Chorismate_synth; 1.
CC Prodom: PD002941; Chorismate_synth; 1.
CC Trifram: TRGR00033; aroc; 1.
CC
CC PROSITE: PS00787; CHORISMATE SYNTHASE_1; 1.
CC PROSITE: PS00788; CHORISMATE SYNTHASE_2; 1.
CC PROSITE: PS00789; CHORISMATE SYNTHASE_3; 1.
CC
CC KW Lyase; Aromatic amino acid biosynthesis; Complete proteome.
CC
CC SO SEQUENCE 357 AA; 38691 MW; 4504562BADF68164 CRC64;

```

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Query Match 45.5%; Score 5; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 CPDSE 8
    |||||
Db 185 CPDSE 189

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```

RESULT 14
DUT_HSV7J STANDARD; PRT; 379 AA.
ID DUT_HSV7J
AC P52341;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
DE (DUTPase) (dUTP pyrophosphatase).
GN U45.
OS Human herpesvirus (type 7 / strain J1) (HHV7).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=57278;
RP SEQUENCE FROM N.A.
RA Nicholas J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT
CC PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES
CC AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
CC URACIL CANNOT BE INCORPORATED INTO DNA.
CC -1- CATALYTIC ACTIVITY: dUTP + H(2)O -> dUMP + diphosphate.
CC -1- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
CC -----
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CC -----
CC
CC EMBL: UA3400; AAC54707.1; -
CC InterPro: IPR001428; DeoxyUTPase.
CC Pfam: PF00692; dUTPase; 1.
CC KW Hydrolyase; Nucleotide metabolism.
CC
CC SO SEQUENCE 379 AA; 43876 MW; 56C61E097B67AD7C CRC64;

```

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Query Match 45.5%; Score 5; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 DCPDE 7
    |||||
Db 287 DCPDE 291

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RESULT 15
YAZ1_SCHPO STANDARD; PRT; 431 AA.
ID YAZ1_SCHPO
AC Q10223;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C13D6.01 in chromosome I.
GN SPAC13D6.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RP SEQUENCE FROM N.A.
PC SPRAIN-972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs W., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambolt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Snpakovski G.V., Ussey D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
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CC -----
CC EMBL: Z69725; CAA93541.1; -
CC Hypothetical protein.
CC KW
CC SO SEQUENCE 431 AA; 49623 MW; 132PB0919646AC9F CRC64;

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Query Match 45.5%; Score 5; DB 1; Length 431;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 DCPDE 7  
11111  
DB 171 DCPDE 175  
Search completed: April 16, 2003, 16:35:28  
Job time : 4.55993 secs

---

GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: April 16, 2003, 16:18:40 ; Search time 0.614121 Seconds  
(without alignments)  
527.016 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66

Sequence: 1 FVDCPDESMAL 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

## Database :

Issued Patents, AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	579	4	US-09-643-597-176
2	66	100.0	579	4	US-09-643-597-348
3	59	89.4	577	4	US-09-261-855-2
4	40	60.6	309	3	US-09-109-205-1
5	38	57.6	398	1	US-08-261-822A-16
6	38	57.6	398	5	PCR-US95-07744A-16
7	38	57.6	826	4	US-09-564-805-2
8	38	57.6	826	4	US-09-564-805-224
9	38	57.6	826	4	US-09-564-805-226
10	37	56.1	430	4	US-09-149-476-707
11	37	56.1	822	4	US-09-564-805-222
12	37	56.1	885	4	US-09-342-648-9
13	37	56.1	1044	2	US-08-777-405A-2
14	37	56.1	1044	2	US-08-977-871A-2
15	37	56.1	1044	2	US-08-925-951-2
16	36	54.5	120	1	US-08-542-363-26
17	36	54.5	120	4	US-09-100-089-26
18	36	54.5	120	4	US-09-670-827-26
19	36	54.5	269	4	US-09-082-649B-82
20	36	54.5	271	1	US-07-977-630-5
21	36	54.5	271	1	US-08-850-880-6
22	36	54.5	271	2	US-08-944-916-6
23	36	54.5	271	2	US-08-814-877-6
24	36	54.5	271	4	US-08-760-615-8
25	36	54.5	271	4	US-09-131-028A-5
26	36	54.5	271	4	US-09-131-028A-7
27	36	54.5	271	4	US-09-272-432A-6

28	36	54.5	274	2	US-08-469-537A-55	Sequence 55, Appl
29	36	54.5	275	2	US-07-857-224B-71	Sequence 71, Appl
30	36	54.5	293	2	US-08-701-191A-26	Sequence 26, Appl
31	36	54.5	523	3	US-08-651-999A-2	Sequence 2, Appl
32	36	54.5	523	4	US-09-385-752-2	Sequence 2, Appl
33	36	54.5	837	4	US-09-564-805-228	Sequence 228, App
34	36	54.5	1255	3	US-08-947-823-3	Sequence 3, Appl
35	36	54.5	1257	3	US-08-947-823-5	Sequence 5, Appl
36	36	54.5	1614	4	US-09-052-469-2	Sequence 2, Appl
37	36	54.5	2213	1	US-08-727-034-3	Sequence 3, Appl
38	36	54.5	2214	1	US-08-727-034-7	Sequence 7, Appl
39	36	54.5	4302	3	US-08-658-136-5	Sequence 5, Appl
40	36	54.5	4302	4	US-09-052-469-8	Sequence 8, Appl
41	36	54.5	4303	2	US-08-460-751-2	Sequence 2, Appl
42	36	54.5	4339	4	US-09-052-469-6	Sequence 6, Appl
43	35.5	53.8	566	3	US-08-335-865J-9	Sequence 9, Appl
44	35.5	53.8	593	3	US-08-335-865J-21	Sequence 21, Appl
45	35	53.0	288	1	US-08-396-650-1	Sequence 1, Appl

## ALIGNMENTS

```

RESULT 1
US-09-643-597-176
Sequence 176, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-176

Query Match      100.0%; Score 66; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 FVDCPDESMAL 11
Db      41 FVDCPDESMAL 51

RESULT 2
US-09-643-597-348
Sequence 348, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.

```

APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-348

Query Match  
Best Local Similarity 100.0%; Score 66; DB 4; Length 579;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDPSMAL 11  
DB 41 FVDCPDPSMAL 51

RESULT 3  
US-09-261-855-2  
Sequence 2, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261,855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-2

Query Match  
Best Local Similarity 81.8%; Score 59; DB 4; Length 577;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FVDCPDPSMAL 11  
DB 41 FVDCPDPSMAL 51

RESULT 4  
US-09-109-205-1  
Sequence 1, Application US/09109205  
Patent No. 6057140  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Guegler, Karl J.  
APPLICANT: Gorgone, Gina  
APPLICANT: Corley, Neil C.  
APPLICANT: Baughn, Mariah R.  
APPLICANT: Yue, Henry  
TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,205  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0542 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT14  
CLONE: 1511003  
US-09-109-205-1

Query Match  
Best Local Similarity 60.6%; Score 40; DB 3; Length 309;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDPE 7  
DB 134 FVDCPDPE 140

RESULT 5  
US-08-261-822A-16  
Sequence 16, Application US/08261822A  
Patent No. 5650553  
GENERAL INFORMATION:  
APPLICANT: Ecker, Joseph R. et al.  
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene  
NUMBER OF SEQUENCES: 82  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 565053315  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,822A  
FILING DATE: 17-JUN-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardsell, Lori Y.  
REGISTRATION NUMBER: 34,293  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 16:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-261-822A-16

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Query Match          57.6%; Score 38; DB 1; Length 398;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 VDCPDSESWAL 11
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Db 245 FLEYPPESWAV 255

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RESULT 6
PCT-US95-07744A-16
; Sequence 16, Application PC/TUS9507744A
; GENERAL INFORMATION:
; APPLICANT: Trustees of The University of Pennsylvania
; TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07744A
; FILING DATE: 15-JUNE-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/261,822
; FILING DATE: June 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Beargell, Lori Y.
; REGISTRATION NUMBER: 34,293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEtical: NO
; ANTI-SENSE: NO
PCT-US95-07744A-16

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Query Match          57.6%; Score 38; DB 5; Length 398;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 VDCPDSESWAL 11
    1:1:11111:
Db 245 FLEYPPESWAV 255

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RESULT 7

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US-09-564-805-2
; Sequence 2, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-805-2

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Query Match          57.6%; Score 38; DB 4; Length 826;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 2 VDCPDSESW 9
    1:11111:
Db 309 VECPDSESF 316

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RESULT 8
US-09-564-805-224
; Sequence 224, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 224
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-564-805-224

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Query Match          57.6%; Score 38; DB 4; Length 826;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 2 VDCPDSESW 9
    1:11111:
Db 309 VECPDSESF 316

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RESULT 9  
US-09-564-805-226

Thu Apr 17 07:55:20 2003

us-09-897-778-176\_copy\_41\_51.ra1

Page 4

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Sequence 226, Application US/09564805
Patent No. 633403
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
NUMBER OF SEQ. ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO 826
LENGTH 826
TYPE: PRT
ORGANISM: Gorilla gorilla
US-09-564-805-226

Query Match 57.6%; Score 38; DB 4; Length 826;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPDESW 9
DB 309 VECPESEF 316

RESULT 10
US-09-149-476-707
Sequence 707, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002p1
CURRENT APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,911
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; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
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; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
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; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
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; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
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; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          56.1%; Score 37; DB 4; Length 430;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      4 CPDESW 9
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Db      19 CPDESW 24

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RESULT 11
US-09-564-805-222
; Sequence 222, Application US/09564805
; Patent No. 633403
; GENERAL INFORMATION:
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 822
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-805-222

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Query Match          56.1%; Score 37; DB 4; Length 822;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 VDCPESMAL 11
      |:||||: |
Db      296 VECPESEFIL 305

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RESULT 12
US-09-342-648-9
; Sequence 9, Application US/09342648
; Patent No. 6248584
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Transcription Coactivators
; FILE REFERENCE: BB-1169-B

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Thu Apr 17 07:55:20 2003

us-09-897-778-176\_copy\_41\_51.ra1

Page: 6

;; CURRENT APPLICATION NUMBER: US/09/342,648  
;; CURRENT FILING DATE: 1999-06-29  
;; EARLIER APPLICATION NUMBER: 60/092,659  
;; EARLIER FILING DATE: July 13, 1998  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 9  
;; LENGTH: 885  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-342-648-9

Query Match 56.1%; Score 37; DB 4; Length 885;  
Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DCPDESWA 10  
DB 47 DTPDEPWA 54

RESULT 13  
US-08-777-405A-2  
; Sequence 2, Application US/0877405A  
; Patent No. 5858753  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,405A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5858753and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1044 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-777-405A-2

Query Match 56.1%; Score 37; DB 2; Length 1044;  
Best Local Similarity 75.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VDCPDESW 9  
DB 5 VDCPMEFW 12

RESULT 14

US-08-977-871A-2  
; Sequence 2, Application US/08977871A  
; Patent No. 5882910  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5882910el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
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; APPLICATION NUMBER: US/08/977,871A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/777,405  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5882910and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1044 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-977-871A-2

Query Match 56.1%; Score 37; DB 2; Length 1044;  
Best Local Similarity 75.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VDCPDESW 9  
DB 5 VDCPMEFW 12

RESULT 15  
US-09-225-951-2  
; Sequence 2, Application US/09225951  
; Patent No. 5985589  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5985589el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; SOFTWARE: IBM PC compatible  
US-09-225-951-2

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,951  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5985589and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1044 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-225-951-2

Query Match 56.1%; Score 37; DB 2; Length 1044;  
Best Local Similarity .75.0%; Pred. NO. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Caps 0;  
QY 2 VDCPDSEW 9  
| | | | |  
DB 5 VDCPMEFW 12

Search completed: April 16, 2003, 16:22:59  
Job time : 1.61412 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:21:35 ; Search time 0.83087 Seconds  
(without alignments)  
1001.062 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66  
Sequence: 1 FVDCPDSESWAL 11

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEM\_PUB pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEM\_PUB pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEM\_PUB pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEM\_PUB pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	10	US-09-897-778-466 Sequence 466, App
2	66	100.0	18	10	US-09-897-778-465 Sequence 465, App
3	66	100.0	20	10	US-09-735-705-400 Sequence 400, App
4	66	100.0	20	10	US-09-850-716A-400 Sequence 400, App
5	66	100.0	20	10	US-09-897-778-400 Sequence 400, App
6	66	100.0	20	10	US-09-897-778-457 Sequence 457, App
7	66	100.0	579	10	US-09-735-705-116 Sequence 116, App
8	66	100.0	579	10	US-09-735-705-348 Sequence 348, App
9	66	100.0	579	10	US-09-850-716A-176 Sequence 176, App
10	66	100.0	579	10	US-09-850-716A-348 Sequence 348, App
11	66	100.0	579	10	US-09-897-778-176 Sequence 176, App
12	66	100.0	579	10	US-09-897-778-348 Sequence 348, App
13	66	100.0	579	10	US-09-897-778-446 Sequence 446, App
14	66	100.0	579	10	US-09-897-778-449 Sequence 449, App
15	66	100.0	586	10	US-09-850-716A-427 Sequence 427, App
16	66	100.0	586	10	US-09-897-778-427 Sequence 427, App
17	59	89.4	577	10	US-09-873-637-2 Sequence 2, Appl1
18	58	87.9	20	10	US-09-735-705-399 Sequence 399, App
19	58	87.9	20	10	US-09-850-716A-399 Sequence 399, App

20	58	87.9	20	10	US-09-897-778-399 Sequence 399, App
21	47	71.2	620	10	US-09-764-864-1116 Sequence 1116, App
22	41	62.1	52	9	US-09-796-692-1087 Sequence 1087, App
23	41	62.1	52	9	US-09-796-692-1561 Sequence 1561, App
24	41	62.1	60	9	US-09-796-692-878 Sequence 878, App
25	41	62.1	68	9	US-09-796-692-687 Sequence 687, App
26	41	62.1	76	9	US-09-796-692-1076 Sequence 1076, App
27	41	62.1	82	9	US-09-796-692-1641 Sequence 1641, App
28	40	60.6	303	9	US-09-925-299-851 Sequence 851, App
29	40	60.6	303	10	US-09-925-299-851 Sequence 851, App
30	38	57.6	826	9	US-09-988-626-2 Sequence 2, Appl1
31	38	57.6	826	9	US-09-988-626-224 Sequence 224, App
32	38	57.6	826	9	US-09-988-626-226 Sequence 226, App
33	38	57.6	826	9	US-09-988-687-2 Sequence 2, Appl1
34	38	57.6	826	9	US-09-988-687-224 Sequence 224, App
35	38	57.6	826	9	US-09-988-687-226 Sequence 226, App
36	37	56.1	430	9	US-09-988-687-226 Sequence 226, App
37	37	56.1	430	9	US-09-988-687-226 Sequence 226, App
38	37	56.1	822	9	US-09-988-687-222 Sequence 222, App
39	37	56.1	822	9	US-09-988-687-222 Sequence 222, App
40	37	56.1	1044	9	US-10-028-072-234 Sequence 234, App
41	37	56.1	1160	9	US-10-028-072-234 Sequence 234, App
42	37	56.1	1160	9	US-10-121-049-234 Sequence 234, App
43	37	56.1	1160	9	US-10-123-904-234 Sequence 234, App
44	37	56.1	1160	9	US-10-140-470-234 Sequence 234, App
45	37	56.1	1160	9	US-10-175-746-234 Sequence 234, App

#### ALIGNMENTS

RESULT 1  
US-09-897-778-466  
Sequence 466, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.453C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-466  
Query Match  
Best Local Similarity 100.0%; Score 66; DB 10; Length 11;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVDCPDSESWAL 11  
DB 1 FVDCPDSESWAL 11  
RESULT 2  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong

```
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 2001-06-28
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465
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Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 FVDCPDSESWAL 11
Db 5 FVDCPDSESWAL 15
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RESULT 3
US-09-735-705-400
; Sequence 400, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Katos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-400
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```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```
RESULT 4
US-09-850-716A-400
; Sequence 400, Application US/09850716A
; Patent No. US20020115139A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Katos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; NUMBER OF SEQ ID NOS: 2001-05-07
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-400
```

```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```
RESULT 5
US-09-897-778-400
; Sequence 400, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 2001-06-28
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-400
```

```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```
RESULT 6
US-09-897-778-457
; Sequence 457, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
```

```

: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-457

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESML 11
DB 2 FVDCPDESML 12

RESULT 7
US-09-735-705-176
: Sequence 176, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-176

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 579;
Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESML 11
DB 41 FVDCPDESML 51

RESULT 8
US-09-735-705-348
: Sequence 348, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
```

```

: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-348

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 579;
Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESML 11
DB 41 FVDCPDESML 51

RESULT 9
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 579;
Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESML 11
DB 41 FVDCPDESML 51

RESULT 10
US-09-850-716A-348
: Sequence 348, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
```

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; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FVDCPDSESWAL 11
Db      41 FVDCPDSESWAL 51

RESULT 11
US-09-897-778-176
; Sequence 176, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-176

Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FVDCPDSESWAL 11
Db      41 FVDCPDSESWAL 51

RESULT 12
US-09-897-778-348
; Sequence 348, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FVDCPDSESWAL 11
Db      41 FVDCPDSESWAL 51

RESULT 13
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446

Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FVDCPDSESWAL 11
Db      41 FVDCPDSESWAL 51

RESULT 14
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 449  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-449

Query Match 100.0%; Score 66; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0.0042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||||  
DB 41 FVDCPDESMA 51

RESULT 15  
US-09-850-716A-427  
Sequence 427, Application US/09850716A  
Patent No. US20020115139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 427  
LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-427

Query Match 100.0%; Score 66; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||||  
DB 48 FVDCPDESMA 58

Search completed: April 16, 2003, 16:32:09  
Job time : 1.83087 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:19:20 : Search time 7.38752 Seconds  
(Without alignments)  
960.006 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66  
Sequence: 1 FVDCPDSSMAL 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep:\*  
22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep:\*  
24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
27: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	1	PCT-US01-47576-466
2	66	100.0	11	22	US-09-897-778-466
3	66	100.0	11	24	US-10-007-700-466
4	66	100.0	11	25	US-10-117-982-466
5	66	100.0	18	1	PCT-US01-47576-465
6	66	100.0	18	22	US-09-897-778-465

7	66	100.0	18	24	US-10-007-700-465	Sequence 465, App
8	66	100.0	18	25	US-10-117-982-465	Sequence 465, App
9	66	100.0	20	1	PCT-US01-47576-400	Sequence 400, App
10	66	100.0	20	1	PCT-US01-47576-457	Sequence 457, App
11	66	100.0	20	21	US-09-735-705-400	Sequence 400, App
12	66	100.0	20	22	US-09-850-716-400	Sequence 400, App
13	66	100.0	20	22	US-09-850-716A-400	Sequence 400, App
14	66	100.0	20	22	US-09-897-778-400	Sequence 400, App
15	66	100.0	20	22	US-09-897-778-457	Sequence 457, App
16	66	100.0	20	24	US-10-007-700-400	Sequence 400, App
17	66	100.0	20	24	US-10-007-700-457	Sequence 457, App
18	66	100.0	20	25	US-10-117-982-400	Sequence 400, App
19	66	100.0	20	25	US-10-117-982-457	Sequence 457, App
20	66	100.0	43	25	US-10-117-982-482	Sequence 482, App
21	66	100.0	579	1	PCT-US01-47576-176	Sequence 176, App
22	66	100.0	579	1	PCT-US01-47576-348	Sequence 348, App
23	66	100.0	579	1	PCT-US01-47576-446	Sequence 446, App
24	66	100.0	579	18	PCT-US01-47576-449	Sequence 449, App
25	66	100.0	579	18	US-09-466-396A-176	Sequence 176, App
26	66	100.0	579	18	US-09-476-496A-176	Sequence 176, App
27	66	100.0	579	18	US-09-480-884A-176	Sequence 176, App
28	66	100.0	579	19	US-09-510-376A-176	Sequence 176, App
29	66	100.0	579	19	US-09-542-615A-176	Sequence 176, App
30	66	100.0	579	19	US-09-542-615A-348	Sequence 348, App
31	66	100.0	579	20	US-09-606-421A-176	Sequence 176, App
32	66	100.0	579	20	US-09-606-421B-176	Sequence 176, App
33	66	100.0	579	20	US-09-606-421B-348	Sequence 348, App
34	66	100.0	579	20	US-09-606-421B-176	Sequence 176, App
35	66	100.0	579	20	US-09-630-940A-176	Sequence 176, App
36	66	100.0	579	20	US-09-630-940A-348	Sequence 348, App
37	66	100.0	579	20	US-09-630-940B-176	Sequence 176, App
38	66	100.0	579	20	US-09-630-940B-348	Sequence 348, App
39	66	100.0	579	20	US-09-662-786-176	Sequence 176, App
40	66	100.0	579	20	US-09-662-786-348	Sequence 348, App
41	66	100.0	579	20	US-09-685-696-176	Sequence 176, App
42	66	100.0	579	20	US-09-685-696-348	Sequence 348, App
43	66	100.0	579	21	US-09-735-705-176	Sequence 176, App
44	66	100.0	579	21	US-09-735-705-348	Sequence 348, App
45	66	100.0	579	21	US-09-791-537-45019	Sequence 45019, A

#### ALIGNMENTS

RESULT 1  
PCT-US01-47576-466  
Sequence 466, Application PC/TUS0147576  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tongtong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retler, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Matanabe, Yoshinori  
APPLICANT: Peckman, David W.  
APPLICANT: Cal, Feng  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.45503PC  
CURRENT APPLICATION NUMBER: PCT/US01/47576  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FASTSEQ for Windows Version 4.0

```

; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-466
Query Match      100.0%; Score 66; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 2
US-09-897-778-466
; Sequence 466, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Beckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-466
Query Match      100.0%; Score 66; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 3
US-10-007-700-466
; Sequence 466, Application US/10007700
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-466
Query Match      100.0%; Score 66; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 4
US-10-117-982-466
; Sequence 466, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-466
Query Match      100.0%; Score 66; DB 25; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 5
PCT-US01-47576-465
; Sequence 465, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
```

```

; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-466
Query Match      100.0%; Score 66; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 4
US-10-117-982-466
; Sequence 466, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-466
Query Match      100.0%; Score 66; DB 25; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 5
PCT-US01-47576-465
; Sequence 465, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
```

```

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-465

```

```

Query Match          100.0%; Score 66; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15

```

## RESULT 6

```

US-09-897-778-465
; Sequence 465, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455016
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465

```

```

Query Match          100.0%; Score 66; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15

```

## RESULT 7

```

US-10-007-700-465
; Sequence 465, Application US/10007700
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.

```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455017
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-465

```

```

Query Match          100.0%; Score 66; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15

```

## RESULT 8

```

US-10-117-982-465
; Sequence 465, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455018
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-465

```

```

Query Match          100.0%; Score 66; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15

```

## RESULT 9

```

PCT-US01-47576-400
; Sequence 400, Application PC/TUS0147576

```

```

: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tonglong
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Veddyck, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Peckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT

: ORGANISM: Homo sapiens
: PCT-US01-47576-400

Query Match
Best Local Similarity 100.0%; Score 66; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESWAL 11
Db 2 FVDCPDESWAL 12

RESULT 10
PCT-US01-47576-457
: Sequence 457, Application PC/TUS0147576
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tonglong
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Veddyck, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Peckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT
```

```

: ORGANISM: Homo sapiens
: PCT-US01-47576-457

Query Match
Best Local Similarity 100.0%; Score 66; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESWAL 11
Db 2 FVDCPDESWAL 12

RESULT 11
US-09-735-705-400
: Sequence 400, Application US/09735705
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 400
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-735-705-400

Query Match
Best Local Similarity 100.0%; Score 66; DB 21; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESWAL 11
Db 2 FVDCPDESWAL 12

RESULT 12
US-09-850-716-400
: Sequence 400, Application US/09850716
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716-400
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Query Match          100.0%; Score 66; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 FVDCPDESMAL 11
        |||
Db       2 FVDCPDESMAL 12
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RESULT 13
US-09-850-716A-400
; Sequence 400, Application US/09850716A
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-400
```

```
Query Match          100.0%; Score 66; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESMAL 11
        |||
Db       2 FVDCPDESMAL 12
```

```
RESULT 14
US-09-897-778-400
; Sequence 400, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-400
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```
Query Match          100.0%; Score 66; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0019;
```

```
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 FVDCPDESMAL 11
        |||
Db       2 FVDCPDESMAL 12
```

```
RESULT 15
US-09-897-778-457
; Sequence 457, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-457
```

```
Query Match          100.0%; Score 66; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESMAL 11
        |||
Db       2 FVDCPDESMAL 12
```

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Search completed: April 16, 2003, 16:29:54
Job time : 7.38752 secs
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GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Comugen Ltd.

OK protein - protein search, using sw model

Run on: April 16, 2003, 16:19:55 ; Search time 1.35468 Seconds  
(without alignments)  
1266.170 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66

Sequence: 1 FVDCPDSESMAL 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 705215 seqs, 155932251 residues

705215

## ALIGNMENTS

27	59	89.4	598	5	US-09-724-676-48616	Sequence 48616, A
28	59	89.4	598	5	US-09-724-676-48621	Sequence 48621, A
29	59	89.4	598	5	US-09-724-676-48616	Sequence 48616, A
30	59	89.4	598	5	US-09-724-676-48621	Sequence 48621, A
31	59	89.4	602	5	US-09-724-676-48619	Sequence 48619, A
32	59	89.4	602	5	US-09-724-676-48620	Sequence 48620, A
33	59	89.4	602	5	US-09-724-676-48619	Sequence 48619, A
34	59	89.4	602	5	US-09-724-676-48620	Sequence 48620, A
35	58	87.9	20	6	US-10-313-986-399	Sequence 399, App
36	58	87.9	20	6	US-10-313-986-470	Sequence 470, App
37	58	87.9	20	6	US-10-313-986-507	Sequence 507, App
38	47	71.2	97	5	US-09-513-999C-7342	Sequence 7342, Ap
39	47	71.2	255	7	US-60-452-680-15601	Sequence 15601, A
40	47	71.2	555	1	PCT-US02-31357-40	Sequence 40, Appl
41	47	71.2	555	6	US-10-262-445-40	Sequence 40, Appl
42	47	71.2	556	7	US-60-453-135-11528	Sequence 11528, A
43	47	71.2	556	7	US-60-453-050-11528	Sequence 11528, A
44	47	71.2	587	6	US-10-313-986-501	Sequence 501, App
45	47	71.2	599	7	US-60-453-135-11527	Sequence 11527, A

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA, New: \*

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2: /cgn2.6/ptodata/1/paa/US07\_NEW.COMB.pep: \*

3: /cgn2.6/ptodata/1/paa/US08\_NEW.COMB.pep: \*

4: /cgn2.6/ptodata/1/paa/US09\_NEW.COMB.pep: \*

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6: /cgn2.6/ptodata/1/paa/US60\_NEW.COMB.pep: \*

7: /cgn2.6/ptodata/1/paa/US60\_NEW.COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	US-10-313-986-466	Sequence 466, App
2	66	100.0	18	US-10-313-986-465	Sequence 465, App
3	66	100.0	20	US-10-313-986-400	Sequence 400, App
4	66	100.0	20	US-10-313-986-457	Sequence 457, App
5	66	100.0	20	US-10-313-986-508	Sequence 508, App
6	66	100.0	43	US-10-313-986-482	Sequence 482, App
7	66	100.0	134	US-09-724-676-92917	Sequence 92917, A
8	66	100.0	134	US-09-724-676-92917	Sequence 92917, A
9	66	100.0	492	US-09-724-676-92916	Sequence 92916, A
10	66	100.0	492	US-09-724-676-92916	Sequence 92916, A
11	66	100.0	558	US-09-724-676-92918	Sequence 92918, A
12	66	100.0	558	US-09-724-676-92918	Sequence 92918, A
13	66	100.0	579	US-10-313-986-176	Sequence 176, App
14	66	100.0	579	US-10-313-986-348	Sequence 348, App
15	66	100.0	579	US-10-313-986-446	Sequence 446, App
16	66	100.0	579	US-10-313-986-449	Sequence 449, App
17	66	100.0	579	US-10-313-986-480	Sequence 480, App
18	66	100.0	579	US-10-313-986-484	Sequence 484, App
19	66	100.0	579	US-10-313-986-484	Sequence 484, App
20	66	100.0	589	US-10-313-986-427	Sequence 427, App
21	66	100.0	589	US-10-313-986-427	Sequence 427, App
22	59	89.4	572	US-09-724-676-48617	Sequence 48617, A
23	59	89.4	572	US-09-724-676-48617	Sequence 48617, A
24	59	89.4	572	US-09-724-676-48617	Sequence 48617, A
25	59	89.4	572	US-09-724-676-48617	Sequence 48617, A
26	59	89.4	577	US-10-313-986-500	Sequence 500, App

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RESULT 1
US-10-313-986-466
Sequence 466, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tonglong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C19
CURRENT FILING DATE: 2002-12-04
CURRENT APPLICATION NUMBER: US/10/313.986
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 466
LENGTH: 11
ORGANISM: Homo sapiens
Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 FVDCPDSESMAL 11
RESULT 2
US-10-313-986-465
Sequence 465, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tonglong
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 465
LENGTH: 18

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Thu Apr 17 07:55:21 2003

us-09-897-778-176\_copy\_41\_51.rapn

Page 2

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-465

Query Match 100.0%; Score 66; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 5 FVDCPDESVAL 15

RESULT 3  
US-10-313-986-400

Sequence 400, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C19  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT APPLICATION NUMBER: US/10/313,986  
CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 400  
LENGTH: 20

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-400

Query Match 100.0%; Score 66; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 2 FVDCPDESVAL 12

RESULT 4  
US-10-313-986-457

Sequence 457, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C19  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT APPLICATION NUMBER: US/10/313,986  
CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 457  
LENGTH: 20

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-457

Query Match 100.0%; Score 66; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 2 FVDCPDESVAL 12

RESULT 5

US-10-313-986-508  
Sequence 508, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C19  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT APPLICATION NUMBER: US/10/313,986  
CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 508  
LENGTH: 20

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-508

Query Match 100.0%; Score 66; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 2 FVDCPDESVAL 12

RESULT 6  
US-10-313-986-482

Sequence 482, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C19  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT APPLICATION NUMBER: US/10/313,986  
CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 482  
LENGTH: 43

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-482

Query Match 100.0%; Score 66; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 9 FVDCPDESVAL 19

RESULT 7  
US-09-724-676-92917

Sequence 92917, Application US/09724676  
GENERAL INFORMATION:

APPLICANT: Compugen LTD.  
APPLICANT: Compugen LTD.

APPLICANT: Variants of alternative splicing  
TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92917

Query Match 100.0%; Score 66; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 8  
US-09-724-676A-92917  
Sequence 92917, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92917

Query Match 100.0%; Score 66; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 9  
US-09-724-676-92916  
Sequence 92916, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92916

Query Match 100.0%; Score 66; DB 5; Length 492;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 10  
US-09-724-676A-92916  
Sequence 92916, Application US/09724676A  
GENERAL INFORMATION:

APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92916

Query Match 100.0%; Score 66; DB 5; Length 492;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 11  
US-09-724-676-92918  
Sequence 92918, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92918

Query Match 100.0%; Score 66; DB 5; Length 558;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 12  
US-09-724-676A-92918  
Sequence 92918, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92918

Query Match 100.0%; Score 66; DB 5; Length 558;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

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RESULT 13
US-10-313-986-176
; Sequence 176, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

RESULT 14
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

RESULT 15
US-10-313-986-446
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-446

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

Search completed: April 16, 2003, 16:31:16
Job time : 2.35466 secs

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